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am09e08.sl Soares_NFL_T_GBC_Sl Homo
IMAGE:1466342 3', mRNA sequence.
AA897178
AA897178.1 GI:3033798
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 847 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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                                                                                                      /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized. Idbraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the arms a liberation when the consistered of the consiste
from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239; 726408-728711, and 72906-731399. Subtraction by Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1466342"
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Primates;
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ae80c02.sl Stratagene schizo brain
IMAGE:970466 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further possible reversed clone: polyT not found seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         White,Y., Wylie,T., WashU-NCI human EST Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway,
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/tissue_type="schizophrenic brain S-11 frontal
/dev_stage="34 years old"
                                                                                                                                                                        /clone_lib="Stratagene schizo brain
/sex="male"
                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:970466"
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Maximum Match 100%
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Maximum DB seq
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AZ177954 SP_0148_B
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ALZ16729 Tetraodon
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AZ136212 SP_0188_A
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1083)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: AFCC
Tissue Procurement: AFCC
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AGENCOURT 6481789 NIH_MGC_71 Homo 5', mRNA sequence.
EM476887
EM476887.1 GI:18525929
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informati
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12275 row: j column: 18
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                                                    334
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/db_cref="taxon:9606"
/clone="IMAGE:555541"
/clone="ib="NIH_MGC_71"
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/tissue_typ
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Bouillaud, F.
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EST20108 Clontech adult human
CDNA clone 20108, mRNA sequen
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R17106.1 GI:770716
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Matches 743; Conservative
                                    CTTTATCTGGGAACCCATTTTAAACTGGATAATTGCACAATGTNCAGATTTCCTCTTCGN 308
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Tel: 33 1 45 07 52 87
Fax: 33 1 45 07 58 90
Email: bouillau@infoblogen.fr
Southern human DNA EcoRI single be
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/rissue-type-adipose tissue; lab-host-Bacteriophage
lambda; first strand priming with random and poly-d(T)
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AB018273
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57.4
57.2
                                          Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

Prediction of the coding sequences of unidentified human genes. XI.

The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
DNA Res. 5 (5), 277-286 (1998)
99087487
                                                                                                                                                                                                                                                                      4318 bp
Homo sapiens mRNA for KIAA0730 p
AB018273
2 (bases 1 to 4318)
Ohara,O., Suyama,M.,
Direct Submission
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Homo sapiens adult male brain SK plus clone:hk03632.
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AF193556
AL157766
               Nagase, T.,
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AC023491
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                                                                                                                                   Suyama, M., Kikuno, R., Miyajima, N.,
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                 Ishikawa, K. and Kikuno, R.
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AC024921 Homo sapi
AX344558 Sequence
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AC1074647 Homo sapi
AC108487 Homo sapi
AL139811 Human DNA
AC083801 Homo sapi
AX277865 Sequence
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AC023466 Homo sapi
AC012204 Homo sapi
AC093835 Homo sapi
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AX347143 Sequence
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cocatgaatgatcagaactgacatttaattcatgtttgtctcgccatgcttctttacttt
                                                                   atcamamattyttamamatcattytyttatctaytmytmtmatmattatcygcttatatttc
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Fax:+81-438-52-3914)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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PLIKFRGAQVAPK FKQCDVLQILMTSCPTLPEKATTLSTIKEQEGSDLGPQEQLEQYIN
MLNVALDPPLLKVINGRNIGNITTLDEBUNKTRAKVLRSIYEFLSAEKREFRFQLRG
VAFVMYEDGWKLLKPEEVVINLEYESDFKPYLYKLPLELGTFHQLFKHLGTEDIISYK
QYVEYLSRIFKNSEGKOLDPNEMTVKRVVSGLFRSLQNDSVKYRSDLENVRDLALYL
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KLRPRLLSSILEGLDEETPKVQOFGALCSLQGRLQLLLSSEQFTTGLIRIKKHENDN
AFLANEEKAIRLCKALREGLKVSCFEKLQTTLRVKGFNPIPHSRSETEAFLKRFGNAV
ILLYIQHSOSKOINFLLALAMTLKSATDNLISDTSYLTAMGCNDIYRIGSTQP
KYDSSEPSKLELPMGCTPIPAEHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQP
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APSTPTSFELIFGLLRSIPPLFSGRESHKTSSKHQSFKKLKVNSLPEILKEUTSVE
QAWKLPESERKKIIRLYLKWHEDDKNERNDIA NAVETKILQNEINRLEKQAFLDQNAD
RASRRTFSTSASRFQSDKYSFQRFTSWNQEATSHKSERQQQNKEECPSAGQTYSGR
FFVPPTFKSVONPVEARRWLRQARNISAARNDLHKNAREWVCFKCYLSTKLALAAD
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PNDRFTSEVAMRVMECTACIIIKLENFMQQKV"
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/protein_d="BA34450.1"
/db_xref="gli:3882181"
/translation="YTFMTSWVEFLRNIGLKYILSQQQLLQFAKEISVRANTENWSKE
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/clone_lib="pBluescriptII
/dev_stage="adult"
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/db_xref="taxon:9606"
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Pred. No. 4.7e-92;
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                                             cccatgaatgatcagaactgacatttaattcatgttttgtctcgccatgcttctttacttt
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 12793)
Hudson, T.J., Engert, J. and Richter, A.
Identification of arsacs mutations and methods of use
Patent: WO 0129266-A 1 26-APR-2001;
McGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)
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/db_xref="taxon:9606"
2256 c 2487 g 388
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Copyright (c) 1993 - 2000 Compugen Ltd.
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2 BF650306

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R17106
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AAR97178 am09e08.5

AA776169 ae80c02.5

AA776670 ae80c02.5

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AA770182 wc1-1-BMO-

AW295072 UT-1-BMO-

AW295072 UT-1-BMO-
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R17106 EST20108 C1
BM472954 AGENCOURT
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                                                      AL216729 Tetraodon
AL216729 Tetraodon
BE650306 NEO87D11E
BE650306 NEO87D169 B
AL185191 SP_1004_B
AL185191 SP_0188_A
AL185137 WA758033.X
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BM476887
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AGENCOURT 6481789 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555441
5', mRNA sequence.
BM476887 GI:18525929
BM476887.1 GI:18525929
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo.

Eukaryota; Metazoa; Craniata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1083)

Inpublished (1993)

Unpublished (1999)

Unpublished (1999)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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284
445
616
234
721
1101
1069
936
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/note="Organ: uterus; vector: pCMV-Sporm6; Site_2: SalI; Cloned unidirectionally. primer: Oligo dT
Site_2: SalI; Cloned unidirectionally. primer: Oligo dT
Site_2: SalI; Cloned unidirectionally.
Average insert size 2.1 kb.
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CNS0039G
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BE40138 HTM1-946A
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BE40138 Drosophil
AL106456 Drosophil
AL106395 Drosophil
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                                                                                                                                                                                                                                                                                                                                1234 gttggtgttcgaagtgactggaataacagtttaatgacagcattaatagctcctgcatat 1293
                                                                                                                                                                                                                                                                           667 GTTGAATTGCTAATACAGTTAAAAAAAACGGTATTTCCCTGGTTCTGATCCAACATTATCA
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Best Local Sim:
Matches 765;
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                                                            human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bouillaud, F.
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                                                                                                                                                     R17106
EST20108 Clontech adult 795 bp mRNA linear EST 12-CRA Clone 20108, mRNA sequence.
R17106.1 GI:770716
EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 CACATGGAAAAAATTTCTATTTGTGAAAATAGATAAGAGTACTGGAGCTCTAAATGTGCTG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754 cacatggaaaaatttctatttgtgaaatagataagagtactggagctctaaatgtgctg 813
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08A Homo sapiens
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                                                                                     489 TGTGCTGTATTTCAGTGGNAGGGCCCAAATCACAGATGGAGACAGATTGAAAAGGGAAACA 548
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Best Local Similarity
Matches 743; Conserva
                                                                                                                                                                            369 CAGAATCTTTTGGGACCAANCTGCGCTCAGATGNGGGNCAGAACTTCTAATGTTTCTTAA 428
                                                                                                                                                                                         697 cagaatottttgg--acaaactgcgctcagat--ggggcagaacttctaatgtttcttaa 752
                                                                                                                                                                                                                         309 AATGCAGAAAATGGCAAAAAGTTTCGGAAAATTTCGNCTGTNCCAGCATCAGACAGAATGGNC
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                                                                                                                                                                                                                                                                             577 ctttatctgggaacccattttaaactggataattgcacaatgttcagatttcctcttcgt 636
                                                                                                                                                                                                                                                                                                            189 GGACGCATGTTTAGAGATTTGGATGCAGATTTTAGGACACAGNTCTCAGATGTTCTGGAT 248
                                                                                                                                                                                                                                                                                                                         517 ggacgcatgtttagagatttggatgcagattttaggacacagttctcagatgttctggat 576
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                                              ATTTCATGCATCTGTAATTGATAGTGTTACTAAAAAGAGGCAGCTCNAAGACATACCAGT
                                                                                                                                                                                                                                                                                                                                                         129 ATCCTCTGTGTATTTTNGATCCTCATGCCAGATATGCACCAGGGGCCACATCCATTAGTCCC
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Fax: 33 1 45 07 58 90
Email: bouillau@infobiogen.fr
Southern human DNA EcoRI single band 2
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oligonucleotides."
a 150 c 166 g 216 t 20 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo Sapiens"
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RESULT R17106 LOCUS

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1010 bp mRNA linear EST 05-FEB-2002
AGENCOURT 6466106 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574588
5', mmA sequence.
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1 (bases 1 to 1010)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: Agencourt Bioscience Corporation

DNA Sequencing by: Agencourt Bioscience Corporation information can be

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.lln.
Plate: LLAM12323
                                                                                                                                                                               CAGTTCAACAAATAACCTATACTATGGATACTGAGGACTCTGAAGGAAATCTTACTACGT 79
                                                                                       GGCTAATTTGTAATAGATCAGGCTTTTCAAGTATGGAGAAAGTATCTAAAAGTGTCATAT 139
                                                                                                                ggctaatttgtaatagatcaggcttttcaagtatggagaaagtatctaaaagtgtcatat 1039
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/clone="ImMGE:5574588"

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/clone_lib="Nufl_MGC_88"

/clone_lib="Nufl_MGC_88"

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/note="Organ: small intestine; Vector; pcMy-SpORT6;

/note="Organ: small intestine; Vector indirectionall;

/note="Organ: small intestine; Intestine; Vector indirectionall;

/note="Organ: small intestine; Intestine intestine;

/note="Organ: small intestine; Intestine; Intestine;

/note="Organ: small intestine; Intestine;
/note="Organ: small intestine; Intestine;
/note="Organ: small intestine;
/note="Organ: pcMy-SpORT6;
/note="Organ: pcMy
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                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                              Score 458.4; DB 10;
pred. No. 3e-106;
                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1159
                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 GGGCTGCCATTTCATGTGAATGGCCCACTTTGCACTGGATTCAGCCAGAAGGAACCTGTGG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 CGTGATGATAATGGACTTGGTGTTCGAAGTGACTGGAATAACAGTTTAATGACAGCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1398 aagt 1401
                                                                         BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gggctgccatttcatgtgaatggccactttgcactggattcagccagaaggaacctgtgg 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgtgatgataatggagttggtgttcgaagtgactggaataacagtttaatgacagcatta 1278
Query Match
Best Local Similarity
Matches 370; Conserv
                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 bp mRNA linear EST 14-AUG-2001
AL596565
DKFZP451L0110_r1 451 (synonym: hlcc1) spinal cord Homo sapiens cDNA
CLone DKFZP451L0110 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL596565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL596565.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; 1 to 376)

1 (bases 1 to 376)
                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s. Wiemann@dkfz, heidelberg.de;

Research Center (DKFZ); Email s. Wiemann@dkfz, within the CDNA

Research Center (DKFZ); Email s. Wiemanny) within the CDNA

sequenced by Medigenomix (Martinsried/Germany) within the sequence

sequencing consortium of the German Genome Project. No sl sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wiemann,S
                                                                                                                                                                                                                                                           This clone (DKFZp451L0110) is available at the RZPD in This clone (DKFZp451L0110) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Please Contact the RZPD: Ressourcenzentrum, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Ottenwaelder, B., Obermaler, B., Mewes, H.W., Weil, B. and Wiemann
         24.6%;
milarity 98.4%;
Conservative
                                                                                                   127
                                                                                                                              /organism="Homo sapiens"
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/clone="TbF2P45110110"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:15154261
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                  /note="vector:psport1; Site_1: Not1; Site_2: Sal1" 63 C 19 9
                   score 345.2;
pred. No. 1.9e;
o; Mismatches
                                              .9e-77
                                                                рв 9;
                                                                Length
                                      Indels
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                                                Gaps
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Length 238;

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908 -tcaaagacataccag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTGAAAAGGAAAACAATTTTTCATGCATCTGTAATTGATAGTGGTACTAAAAAAGAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    850 ttgaaaaggaaa--caatttcatgcatctgtaattgatagtgttactaaaaagaggcagc 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ĠĆAĠAĀCTTCTAĀTĠŦŤŦĊŤŦĀĀTCĀCĀTĠĠĀĀĀĀĀŤŤTCŦĀTŦŦŒŢĠĀĀĀŤĀĠĀŤĀĠ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     730 goagaaottotaatgtttottaatcacatggaaaaaatttotatttgtgaaatagataag 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TCTGTTCCAGCATCAGACAGAATGGTCCAGAATCTTTTGGACAAACTGCGCTCAGATGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     670 tctgttccagcatcagacaggatggtccagaatcttttggacaaactgcgctcagatggg 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 132. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 tgcacaatgttccagatttcctcttcgtaatgcagaaatggcaaaagtttcggaaatttcg 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCT-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates;
1 (bases 1 to 238)
                                                                                    /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with indicated polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized vitro. Following HAP purification, this NHT, and B-cell tracer in a subtractive hybridization reaction. The driver from the same 3 libraries. The pools of 5,000 clones made in M.A.G.E. clones 297480-30287, 68583-687239, Soares and M. Fatima Bonaldo. "Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        am09e08.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone
IMAGE:1466342 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA897178.1 GI:3033798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCACAATGTTCAGATTTCCTCTTCGTAATGCAGAAATGGCAAAAGTTTCGGAAATTTCG
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/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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Catarrhini; Hominidae; Homo.
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Best Local Similarity 99.00,
237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
High quality sequence stop: 206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 ACTGGGCTGCCATTTCATGTGAATGGCCACTTTGCACTGGATTCAGCCAGAAGGAACCTG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Wylie, T., Waterston, R. and Wilson, R. Theising, B., Case, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttaatagotoctg 1 601 (11) | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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/dev_stage="34 years old"
/lab_host="SOLR (Kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI: Library
SO% caucasian, 50% Aleutian: Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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ae80c02.s1 Stratagene schizo brain

IMAGE:970466 3', mRNA sequence.
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                                                                                                                                                                                                                                                          /clone_lib="Stratagene schizo brain Sll"
/sex="male"
                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:970466"
                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4.5e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Mart, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Wash D., C. Laman EST Project
                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA776670
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excised.
Material
           tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_Stage="34 years old"
/lab_bost="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Library
/note="Vector: Bluescript SK-; Site_1: EcoRI; Library
/constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised Custom library. Avg insert length 1 4kb.
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Johns Hopkins School of Medicine, Baltimore MD."
a 42 c 47 g 62 t
                                                                                                                                                                  /clone_lib="Stratagene schizo brain S11"
/sex="male"
                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:970514"
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SP_0148_B2_G06_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=148 Col=12 Row=N, DNA sequence.

AZ177954

AZ177954.1 GI:8350329
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 499
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: acameron@caltech.edu
Plate: 148 row: N column:
Seq primer: SP6
Class: BAC ends
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Tel: (626) 395-8421
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California Institute of Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20402566
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(626) 793-3047
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                                                                                    /note="Organ: sperm;
DH10B"
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a 30 c 33 g 48 t
                                                                                                                                            /clone="Plate=148 Col=12 Row=N"
/Clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E
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/db_xref="taxon:7668"\
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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UI-H-BW0-ait-c-04-0-UI.s1 NCI_CGAP_Sub6
IMAGE:2730247 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy
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Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="IMAGE:2730247"
/clone_iib="NCI_CGAP_Sub6"
/clone_lib="NCI_CGAP_Sub6"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="Nector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="label" with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
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                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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     Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 434)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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GI:7040288

Craniata; Vertebrata; Catarrhini; Hominidae,

Homo

sapiens mRNA

CDNA

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422 toacagactgcccatcttttatttctggcaatgacatcctgtgtattttttgatcctca 479
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Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome
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TAG_TISSUE=prostate
TAG_SEQ=AAGTG"

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                                                                                                                                                           CNS02W80 1067 bp DNA linear GS Tetraodon nigroviridis genome survey sequence PUC-Ori 176G09 of library G from Tetraodon nigroviridis, genom
                                                                                                      GSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                        Tetraodon nigroviridis
                                                                                    GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                    AL216729.1
                                                                                                                                    sequence.
AL216729
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Life Technologies catalog #: 11548-013
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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/clone="IMAGE:2832476"
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/db_xref="taxon:99883"
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                        catcttttatttctggcaatgacatcctgtgtattttttgatcctcatgccagatatgcac
                                                                                                  cttataaaactggacagtatggaataggattcaattctgtgtatcatatcacagactgcc
CTTCATTCGTGAGTGGCAAATACTTGGTAT---TGTTTGACCCTCAAGGTGTTTATCTTC
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Epermalophyta; Magnoliophyta; eudicotyledons; core eudic
Spermalophyta; Magnoliophyta; Fabales; Fabaceae; Papilionoideae;
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Insert Length: 586 Std Error: 0.00
Plate: 087 row: D column: 11
Seq primer: TCACACAGGAAACAGCTATGAC.
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/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 an
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 151 c 127 g 171 t 2 others
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/db_xref="taxon:3880"
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agaagatgatgttagaggaattcagaatcttggaaaaggcacgaaagagggaaatcctta
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                                   TCCGGGAATGAAATCTTGTCAGGGACCAGCCCTTTGGGTATACAACGATGCCGTATTCAC
                                                             GGAAGTTCGCTTTCTCATTGACATGAGAAGAAACGTTTTAGAAACCAACAGATTGTTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SP6
Class: BAC ends
High quality sequence stop: 9
Location/Qualifiers
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Proc. Natl. Acad. Sc
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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Fax: (626) 793-3047
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California Institute of Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector:
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/db_xref="taxon:7668"
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Pred. No. 5.7e~11;
0; Mismatches 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGATTGGGAAGTTTGGGACCGGTTTCAACTCGGTGTACCGCATAACTGATGTTCCAAG 439
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                                                                                       aaaggaaatgttgaaagagcttcttcaaaatgctgatgatgcaaaggcgacagaaatctg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ185191 DNA linear SP_1004_B2_D05_T7A Strongylocentrotus purpuratus, sperm genomic BAC library Strongylocentrotus pur clone_Plate=1004_Col=10 Row=H, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cameron, RA, Davidson, EH, Division of Biology 156-29 California Institute of Technology Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends
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Location/Qualifiers
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(626) 793-3047
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                     DH10B" -
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
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/db_xref="taxon:7668"
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cacagaatttgggcagaaagaaaaattgaccagcagaattaagagcatccttaatgcata 143

CACACCAGCTGGGCAACATGAACCCTTGACTATGCGCTTGTGGAATATTCTCAAGAACAA 68

Query Match Best Local S Matches 207

Similarity 51.007; Conservative

0;

Score 80; DB 12; Pred. No. 9.2e-10; 0; Mismatches 187

Length 431 Indels

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VERSION
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431 bp DNA linear G55 3U-AUG-7 SP_0188_Al_A09_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=188 Col=17 Row=A, DNA sequence.
                                                                                                                                                                                                                             Email: acameron@caltech.edu
Plate: 188 row: A column:
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                          Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                           A sea urchin genome project: Sequence scan, virtual map, and additional resources Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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                    126
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Location/Qualifiers
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                  a
                                                  /clone="plate=188 Col=17 Row=A"
/clone_lib="Strongylocentrotus purpuratus, purple
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones 1
                                                                                                                                   /organism="Strongylocentrotus
/db_xref="taxon:7668"
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                                         378 taaaactggacagtatggaataggattcaattctgtgtatcatatcacagactgcccatc 437
                                                               249 AGACCAAGACTTTGAGAATATTCTCCTTCTAGGAGGGCGTACCAAGGAAAAGGACGCTGA 308
                                                                          318 agaagatgatgttagaggaattcagaatcttggaaaaggcacgaaagagggaaatcctta 377
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Search completed: May 22, 2002, 05:31:27 Job time: 4087 sec

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Result
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Perfect score:
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Copyright (c) 1993 - 2000
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R17106 EST20108 C1
AA776670 AGE0902.s
AA897178 AM09608.s
BH157201 ENTSLOTE
AV214110 AV214110
                 BG788610 SEAUMC008
BH034007 RPCI -24-2
B70904 CIT-HSP-206
BG624213 CVEMB-140
AI705955 UI-R-ACO-
AI579360 UI-R-ACO-
BI295731 UI-R-DKO-
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12275 row: j column: 18
High quality sequence stop: 696.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1083)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectonpublished (1999)
Contact: Robert Strausberg, Ph.D.
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AGENCOURT_6481789 NIH_MGC_71 Homo
5', mRNA sequence.
BM476887
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Tissue Procurement: ATCC
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                 /organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homose555441"
/clone=lib="NHH_MGC_71"
/clone_lib="NHH_MGC_71"
/tissue_type="leiomyosarcoma"
/tissue_type="leiomyosarcoma"
/lab_host="PH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Sitsite_2: Sall; Cloned unidirectionally. Prime:
Site_2: Sall; Cloned unidirectionally. Prime:
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A1043792 UI-R-CO-J
A1704578 UI-R-CO-J
A1704578 UI-R-AG1-
BM287243 527562 MA
BE912359 601664865
B1612760 RH41717-MA
BE912355 521174 MA
BE912356 UI-R-BXO-
AQ534831 RPCI-11-3
B1290791 UI-R-DXO-
AC534831 RPCI-11-3
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DKFZp451L0110_r1 451 (synonym: hlcc1)
clone DKFZp451L0110 5', mRNA sequence.
Am Kl
This
                                   Unpublished (2001)
                                                                      Ottenwaelder, B.,
                                                                                                                             EST
                          Contact: Ottenwaelder
                                                               Wiemann,S
                                                                                          Mammalia;
                                                                                                Eukaryota;
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                                                                    karyota; Metazoa; Chordata; C
mmalia; Eutheria; Primates; C
(bases 1 to 376)
tenwaelder,B., Obermaler,B.,
Klopferspitz 18a D-82152
is is the 5' sequence of t
                                                     (Ottenwaelder, B.,
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AGENCOURT_6466106 NIH_MGC_88
5', mRNA sequence
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                                           Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.go
Tissue Procurement: ATCC
                                                                                     1 (bases 1 to 1010)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, 1
Unpublished (1999)
                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                         EST
                                                                                                                                                                                                                      BM472954
BM472954.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin-
                                                                                                                                                                                          human
cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Conso DNA Sequencing by: Agencourt Bioscience Corpo
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/dev_stage="adult"
/lab_host="DH10B"
/note="voct-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp451L0110"
/clone_lib="451 (synonym:
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GERMANY; Email: clo
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IMAGE:5574588
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Best Local Similarity
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IMAGE:970466 3', mRNA sequence.
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Plate: LLAM12323 row: h column:
High quality sequence stop: 738.
                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WashU-NCI human EST Project
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/db_xref="taxon:9606"
/clone="IMAGE:5574588"
/clone=lib="NIH_MGC_88"
/clone=lib="NIH_MGC_88"
/clone=type="duodenal adenocarcinoma, cell line"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="PHIO8 (phage-resistant)"
/note="OGN-FIGURE (phage-resist
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0; Mismatches 1;
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                                                                                                                                                                                                                                    R17106
R17106.1
                                                                                                                                                                                                                                                                                R17106 PST20108 Clontech adult human facouna clone 20108, mRNA sequence.
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 206.
Study of expressed sequences 
Unpublished (1995)
                                            Boulllaud, F.
                                                                               Mammalia; Eutheria; 1 (bases 1 to 795)
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                   human
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Fax: 314 286 1810
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Contact: Wilson RK
                                                                                                                              Eukaryota; Metazoa;
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/dev_stage="34 years old"
/lab_host="$50!R (kanamycin resistant)"
/lab_nost="$50!R (kanamycin resistant)"
/note="vector: Bluescript SK:; Site_1: EcoRI: Library
/sold Standom File Library
/sold Sk: Site_1: EcoRI: EcoRI: Library
/sold Sk: Site_1: EcoRI
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/db_xref="taxon:9606"
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Pred. No. 5.1e-94;
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                                                                            Malmidia..., Jost, Radimidia..., Geisel, G., Jost, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lenon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                          148 bp mRNA lae80g02.s1 Stratagene schizo brain S11 Homo IMAGE:970514 3', mRNA sequence.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
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Southern human DNA EcoRI single band 2.9
Location/Qualifiers
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Centre de Recherche sur l'Endocrinologie moleculaire
                                                                        Unpublished (1997)
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/strain="Caucasian"
/db_xref="taxon:9606"
/clone="20108"
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/note="Vector: lambda gt10; Site_1: EcoRI; dev-stage=adult; tissue-type=adipose tissue; lab_host=Bacteriophage lambda; first strand priming with random and poly-d(T)
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501 cacatccattagtcccggacgcatgtttagagattttggatgcagattttaggacacagtt 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               am09e08.s1 Soai
IMAGE:1466342 :
AA897178
AA897178.1 GI:
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 847 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 131.
Location/Qualifiers
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This clone is available royalty-free through LLNL;
                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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/lab_host="SOLR (kanamycin resistant)"
/note="vector: Bluescript SK-; Site_1: EcoRI; Library
/note="vector: Bluescript SK-; Site_1: EcoRI; Library
/note="vector: Bluescript SK-; Site_1: EcoRI; Library
/note="vector: Bluescript SK-; Site_1: BcoRI; Library
/note="vector: Bluescript Sk-; Site_1: Step I vector: Suicide.
Solvent Stand Into EcoRI site of ZAP II vector. Mass
excised. Custom library. Any insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."

37 a 30 c 33 g 48 t
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/db_xref="taxon:9606"
/clone="IMAGE:970514"
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Soares_NFL_T_GBC_S1 Homo
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Best Local Similarity
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                                                                                                                                                                Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 665)
Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
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Eukaryota; Entamoebidae; Entamoeba.
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ENTSLO5TF Entamoeba histolytica
                                                                                                                                                                                                                             Email: bjloftus@tigr.org
Clones are derived from the
                                                                                                                                                                                                                                                                                          Tel
                                                                                                                                                                                                                                                                                                                                                                        Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Entamoeba histolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH157201.1 GI:15730639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic, DNA sequence.
                                                                                                                                                                                                        DNA library
                                                                                                                                                                                                                                                                   Medical Center Dr., Rockville, 301 838 0208 301 838 3543
                                                                                                   quality sequence start: 18 quality sequence stop: 569 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1466342"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                            /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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/db_xref="taxon:9606"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
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100.0%; Pred. No. 5.2e-62;
'... Mismatches 0;
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SOURCE KEYWORDS

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FEATURES

Carninci,P. and Hayashizaki,Y High-efficiency full-length c

cDNA cloning. Methods Enzymol. 303

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AV214110
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                           Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., IZawa,M., Watahiki,M.,
Matsuura,S., Carninci,P., Muramatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
125 c 82 g 221 t
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su,M., Okazaki,Y. and Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG788610 517 bp mRNA linear EST 20-MAY-2001 SEAUMCO08567 Sea urchin primary mesenchyme cell cDNA library Strongylocentrotus purpuratus cDNA clone PM990802-10-0421 5', mRNA
                                                                                                                               Dept. Biol. Sci.
Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh, PA 15213, USA
Tel: +1 412 268 5849
                                                                                                                                                                                                                               A large scale analysis of mRNAs expressed cells of the sea urchin embryo Development 128 (13), 2615-2627 (2001)
                                                                                                                                                                                                                                                                                                                                Strongylocentrotidae; Strongylocentrotus.
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                                                                                                                                                                                                Contact: Ettensohn CA
                                                                                                                                                                                                                                                                                  Ettensohn, C.A.
                                                                                                                                                                                                                                                                                                Zhu, X., Mahairas, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    further details.
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                                                                                                                                                                                                                                                                                                                   (bases 1 to 517)
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Location/Qualifiers
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/clone="2410133H03"
/clone_11b="RIKEN full-length enriched,
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prepared and sequenced in Mouse Genome Encyclopedia
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/strain="C57BL/6J"
/clone_lib="Sea urchin primary mesenchyme cell cDNA
library"
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/db_xref="taxon:7668"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 267 row: J column: 1
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BH034007
                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
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9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: RPCI-24-267J1.TJ
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/note="Vector: pSPORT1 A+ RNA, directionally cloned"
dt priming from poly A+ RNA, directionally cloned"
a 96 c 176 g 14 t
                                       DNA.
                                                /cell_type="Spleen/Brain"
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/note="Vector: pTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="RPCI-24-267J1"
/clone_lib="RPCI-24"
                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia;
Ostreoidea; Ostreidae; Crassostrea.
                                                                                 CVEMB-140 CVEMB Crassostrea BG624213
                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Other_GSSs: CIT-HSP-2063E16.TR
                                           eastern oyster.
                                                                      BG624213.1
                                                                                                             BG624213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Researc
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Use of a random BAC End Sequence Database for Sequence-Ready Map
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mmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 758)
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301 838 0208
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Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute for Genomic Research Medical Center Dr., Rockville,
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                        /cell_type="Sperm"
/note="wector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="2063E16"
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                                                                                              mRNA sequence
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ne 2063E16, DNA
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97044477
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UI-R-ACO-yl-b-07-0-UI.sl UI-R-ACO Rattus
UI-R-ACO-yl-b-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Jenny MJ
Marine Biomedicine and Environmental
Medical University of South Carolina
221 Fort Johnson Road, Charleston, SC
Tel: 843 876 5058
Fax: 843 762 5530
                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 263-301, >(CAG
                                                                                                                                                                                                                                                 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
Program for Rat Gene
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                discovery
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Gross, P.S. and Bartlett, T.
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                                                                                                    )n#Simple_repeat
Seq primer: M13 Forward
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ilarity 100.0%;
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/tissue_type="Embryo, D-veliger larvae"
/tissue_type="Embryo, D-veliger larvae"
/note="Vector: pTriplEx2; Site_1: Sfi I; Site_2: Sfi I"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/db_xref="taxon:6565"
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                                     /organism="Rattus norvegicus"
                                                                  Location/Qualifiers
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Rodentia;
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/clone="UI-R-ACO-y1-b-07-0-UI" /clone\_lib="UI-R-ACO" /dev\_stage="adult"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 bp mRNA linear EST 05-APR UI-R-AGO-wu-h-08-0-UI.s1 UI-R-AGO Rattus norvegicus cDNA clone UI-R-AGO-wu-h-08-0-UI 3', mRNA sequence.
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University of Iowa
1. Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             elements were found in this cDNA sequence:
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/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-ACO
library is a non-normalized library constructed from 16.5
dpc rat atrioventricular (AV) canal. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_SEQ=None found"

196 Towa.
TAG_SEQ=None found"
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/lab_host-"DH10B (Life Technologies)"
/note-"Vector: pT73D-Pac (Pharmacia) with a modified
/note-"Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AG0
library is a non-normalized library constructed from 13
dpc rat ventricle. The tag is a string of 6 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
                                                                                                                                                                                            /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI.R-AGO"-wu-h-08-0-UI"
/clone_lib="UI-R-AGO"
/dev_stage="adult"
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           Tissue provided by Jim Lin, Department of Biology,
University of Iowa."
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                          20;
                          Conservative
                                   100.0%;
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                                   Score 20;
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                          Mismatches
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VERSION
AXI19931.1 GI:14036678
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Prinates; Catarrhini; Hominidae; Homo.
AUTHORS
AUTHORS
AUTHORS
Identification of arraces mutations and methods of use therefor Journale
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FEATURES
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Location/Qualifiers
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BASE COUNT

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                                                                                                                                                                                                                           ctggataattgcacaatgttcagatttcctcttcgtaatgcagaaatggcaaaagtttcg
                                                                                                                                                                                                                                                                                     aacaaccagccatttacagaagatgatgttagaggaattcagaatcttggaaaaggcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGCTGATGATGCAAAGGCGACAGAAATCTGTTTTGTGTTTGATCCTAGACAGCATCCA
                                                                     GGAGACAGATTGAAAAGGAAACAATTTCATGCATCTGTAATTGATAGTGTTACTAAAAAG
                                                                              ggagacagattgaaaaggaaacaatttcatgcatctgtaattgatagtgttactaaaaag
                                                                                                                  atagataagagtactggagctctaaatgtgctgtattcagtaaagggcaaaatcacagat
                                                                                                                                                    tcagatggggcagaacttctaatgtttcttaatcacatggaaaaaatttctatttgtgaa
                                                                                                                                                                               GAAATTTCGTCTGTTCCAGCATCAGACAGAATGGTCCAGAATCTTTTGGACAAACTGCGC
                                                                                                                                                                                       gaaatttcgtctgttccagcatcagacagaatggtccagaatcttttggacaaactgcgc
                                                                                                                                                                                                                 CTGGATAATTGCACAATGTTCAGATTTCCTCTTCGTAATGCAGAAATGGCAAAAGTTTCG
                                                                                                                                                                                                                                                    GCAGATTTTAGGACACAGTTCTCAGATGTTCTGGATCTTTATCTGGGAACCCATTTTAAA
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                                                                                                         ATAGATAAGAGTACTGGAGCTCTAAATGTGCTGTATTCAGTAAAGGGCCAAAATCACAGAT
                                                                                                                                           TCAGATGGGGCAGAACTTCTAATGTTTCTTAATCACATGGAAAAAATTTCTATTTGTGAA
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AF193556
AF193556.1 G
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Submitted (08-OCT-1999) Genom
1650 Cedar Ave., Montreal, QC
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 12793)
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77. .11566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              General Hospital,
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4163 LKYLKKYGSKILGAVELPSSVKLGFEERGCKOILLENIFSEKOFESEVEFENLOGIEA
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DFSVICQGFFEDIAHGKGKELTKVFSDGSTWVSMKNVRFLDDSILKRRDVGSAAFKIF QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT ACIIIKLENFMQQKV" 1 2256 c 2487 g 3887 t PIPAEIHYTLLMDPMNYFYEGEYVGYLVDAEGGDIYGSXQPTYTYAIIYQEVEREDAD NSSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPEESSQSRDSAPSTPTSPTEELTPGLR SIPPLFSGRESHKTSSKHQSPKKLKVUSLPEILKEVTSVVEQAMKLPESERKKIIRLL YLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSD KYSFQRFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA

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COUNT

Query Match

Best Local Similarity

Matches 1295; Conserv

Conservative

0;

Mismatches

92.4%;

Score 1295; ; Pred. No. 0;

DΒ 9 0;

Length 12793; Indels

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밁 Qy 밁 δõ В QΥ 밁 Qy Вb Qy 밁 Ş Ъ δÃ В Qγ В δõ 밁 Qy В ρ 밁 QΥ 밁 Qy B QY 밁 δÃ Вp δÃ B Qy 맑 δÃ 6440 1141 6320 1021 6260 6200 6140 6080 6020 5960 5900 5840 5780 5720 5660 5600 5540 5480 5420 961 481 421 181 121 901 841 721 661 601 541 361 301 241781 cctctttctttggagactgggctgccatttcatgtgaatggccacttttgcactggattca 1200 aacaaccagccatttacagaagatgatgttagaggaattcagaatcttggaaaaggcacg ggagacagattgaaaaggaaacaatttcatgcatctgtaattgatagtgttactaaaaaag tcagatggggcagaacttctaatgtttcttaatcacatggaaaaaaatttctatttgtgaa 780 gaaatttcgtctgttccagcatcagacagaatggtccagaatcttttggacaaactgcgc ctggataattgcacaatgttcagatttcctcttcgtaatgcagaaatggcaaaagtttcg aatgctgatgatgcaaaggcgacagaaatctgttttgtgttttgatcctagacagcatcca CCTCTTTCTTTGGAGACTGGGCTGCCATTTCATGTGAATGGCCACTTTGCACTGGATTCA GGAGTAGCTGCCTGCATTACTCACAACTATAAAAAACCCCCATAGGGCCTTCTGTTTTTTG | ggagtagctgcctgcattactcacaactataaaaaaccccatagggccttctgtttttttg GTATCTAAAAGTGTCATATCAGCTCACAAGAACCAAGATATTACTCTTTTCCCACGTGGT gtatctaaaagtgtcatatcagctcacaagaaccaagatattactcttttcccacgtggt ATAGATAAGAGTACTGGAGCTCTAAATGTGCTGTATTCAGTAAAGGGCAAAATCACAGAT atagataagagtactggagctctaaatgtgctgtattcagtaaagggcaaaatcacagat TCAGATGGGGCAGAACTTCTAATGTTTCTTAATCACATGGAAAAAATTTCTATTTGTGAA GAAATTTCGTCTGTTCCAGCATCAGACAGAATGGTCCAGAATCTTTTGGACAAACTGCGC CTGGATAATTGCACAATGTTCAGATTTCCTCTTCGTAATGCAGAAATGGCAAAAGTTTCG GCAGATTTTAGGACACAGTTCTCAGATGTTCTGGATCTTTATCTGGGAACCCATTTTAAA gcagattttaggacacagttctcagatgttctggatctttatctgggaacccattttaaa AATGCTGATGATGCAAAGGCGACAGAAATCTGTTTTGTGTTTTGATCCTAGACAGCATCCA 1080 900 600 540 480 6439 6379 6319 1020 6259 960 6199 6139 840 6079 6019 720 5959 660 5899 5839 5779 5719 420 5659 5599 300 240 5479 360

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REFERENCE
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KEYWORDS
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AL157766/c
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, EMBLEDED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gccagaaggaacctgtggcgtgatgataatggagttggtgttcgaagtgactggaataac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-40020 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL157766 92693 bp DNA linear PR Human DNA sequence from clone RP11-40020 on chromosome 13q12.11-12.2, complete sequence.
                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-760Ml is at 92594 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL157766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tromans, A.
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 92693)
                                                                                                                                                                                                                                                                                                             true
                                                                                                                                                                                                                                                                                                                                                                                                                                       //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                       рвасез.6
                                                                                                                                                                                                                                                                                                           right end of clone RP11-72P19
                        /note="MIR repeat: matches
3896, .4201
                                                                                                              /clone_lib="RPCI-11.1" 2390. .2485
                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="13"
  /note="AluY repeat: matches 3.
                                                                                                                                                                           /map="q12.11-12.2"
                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                     note="MIR repeat: matches
                                                                                                                                                      /clone="RP11-40020"
                                                                                                                                                                                                                                                                                       location/Qualifiers
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    .308 of consensus'
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37963...38254
/note="AluSq repeat: matches 9.
38703...39008
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restriction digest data."
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36098. .36415
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/note="Alusg1 repeat: matches 1.
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41322. .41405
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/note="THE1B repeat: matches l. .364 of consensus"
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44790. .45101
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                                                                 'note="AluSx repeat: matches 1. .160 of consensus"
                                                                                                         /evidence=not_experimental
                                                                                                                                /note="CpG island"
                                                                                                                                                                               /note="AluSc
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSq repeat: matches 1.
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                      note="L1MB6 repeat: matches 5822. .6172 of consensus"
                                                                                                                                                                                                                                                                                                           'note≃"AluSx repeat: matches 1. .312 of consensus"
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                                                                           92.4%; Score 1295; I
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                          72454. .72865
/note="MER31-internal repeat: matches 332. .739 of consensus"
72873. .73249
/note="MER31-internal repeat: matches 883. .1261 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSq repeat: matches 1..302 of consensus" 62866. 64385
/note="TIGGER1 repeat: matches 46..1586 of consensus" 64386. 64694
/note="AluX repeat: matches 1..306 of consensus" 64695. 64713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluY repeat: matches 1. .129 of consensus" 62330. .62363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Alusx repeat: matches 1. .305 of consensus" 57331. .57390 /note-"30 copies 2 mer ga 75% conserved" 57357. .57392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Alu repeat; matches 261. .294 of consensus"
62362. .62565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluJo repeat: matches 85. .299 of consensus"
61036    .61144
                                                                                                                                                                                                                                                      consensus"
                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .295 of consensus"
72145. .72256
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/note="MIR repeat: matches 82. .262 of consensus"
58260. .58389
/note="MIR repeat: matches 2. .153 of consensus"
58564. .58611
                                                                                                                                                                                                                                                                      /note="MER31-internal repeat: matches 42.
                                                                                                                                                                                                                                                                                                                                                                          /note="MER21B repeat: matches 548. .680 of consensus"
71411. .71737
                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 1. .311 of consensus"
71279. .71413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluJb repeat: matches 1. .299 of consensus"
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55696. .65717
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55396. .65569
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52566. .62865
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52008. .62187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="10 copies 4 mer tgtg 82% conserved"
7586. 67886
                                                                                                                                                                                                                                                                                                                                                     note="MER31A repeat: matches 47. .485 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 6.
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e="L1PB2 repeat: matches 5789. .6155 of
1. .66410
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1140	ggagtagctgcctgcattactcacaactataaaaaaccccatagggccttctgttttttg	1081	Оу
12471		12530	
1080	gtatctaaaagtgtcatatcagctcacaagaaccaagatattactcttttcccacgtggt	1021	Qy
12531		12590	Db
1020	gaaggaaatcttactacgtggctaatttgtaatagatcaggcttttcaagtatggagaaa	961	Qу
12591		12650	Дъ
960	aggcagctcaaagacataccagttcaacaaataacctatactatggatactgaggactct	901	Оу
12651		12710	
900	ggagacagattgaaaaggaaacaatttcatgcatctgtaattgatagtgttactaaaaag	841	Db Qy
12711		12770	
840	atagataagagtactggagctctaaatgtgctgtattcagtaaagggcaaaatcacagat	781	Оу
12771		12830	
780	tcagatggggcagaacttctaatgtttcttaatcacatggaaaaaatttctatttgtgaa	721	Оу
12831		12890	
720	gaaatttogtctgttccagcatcagacagaatggtccagaatcttttggacaaactgcgc	661	Оу
12891		12950	
660	ctggataattgcacaatgttcagatttcctcttcgtaatgcagaaatggcaaaagtttcg	601	da
12951		13010	VQY
600	gcagattttaggacacagttctcagatgttctggatctttatctgggaacccattttaaa	541	Qy
13011		13070	
540	gccagatatgcaccaggggccacatccattagtcccggacgcatgtttagagatttggat	481	ОУ
13071		13130	ОБ
480	atcacagactgcccatctttatttctggcaatgacatcctgtgtatttttgatcctcat	421	Qy
13131		13190	Db
420	aaagagggaaatcettataaaactggacagtatggaataggattcaattctgtgtatcat	361	Оу
13191		13250	
360 13251	aacaaccagccatttacagaagatgatgttagaggaattcagaatcttggaaaaggcacg	301 13310	Ор
300	gttgatagaatatttgatgataagtgggccccattgcaagggccagcactttgtgtgtac	241	Qy
13311		13370	Db
240	aatgctgatgatgcaaaggcgacagaaatctgttttgtgttttgatcctagacagcatcca	181	Qy
13371		13 <b>43</b> 0	Db
180	attaagagcatccttaatgcatatccttctgaaaaggaaatgttgaaagagcttcttcaa	121	Оу
13431		13490	
120	aatgtctgttttacaacacttggcacagaatttggccagaaagaa	61	Qy
13491		13550	Db

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Homo sapiens chromosome UNK clone
PROGRESS ***, 44 unordered pieces.
AC079761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
Direct Submission
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is
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                            11492 bp
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Identification of arsacs mutations and methods of use therefor
Patent: WO 0129266-A 3 26-APR-2001;
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)
Location/Qualifiers
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                                                         TLFDEMPLIPATLLNEDQTCVELIRLRIPSVVILDDETEAQLPEFLADIVQKLGGIVL
KRLDTSIQHPLVKKYLHSPLSAIIQJMEKIPLQKLCNQIASLLDTHKDALRKFLASL
TDTSEKEKRIJGELTIFKRIMHSSDQGISSYTKLKGCKVLDHTAKLPTDLRLSVSVID
SSDEATIRLANMLKIEKLKTTSCLKFVLKDIGNAFYTQEEVTQLMLWILLENLSSLKNE
                NSNYLDWLMPLKFIHMSQGHYVAAGDLFDPDIEVLRDLFYNEEEEACFPPTIFTSPDIL
HSLRQIGLKNESSLKEKDVYQVARKIEALQVSSCQNQDVLMKKAKTLLLVLNKNQTLL
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2280 c 2387 g 322
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/protein_id="AAF31263.1"
/db_xref="G1:6907044"
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/db_xref="taxon:10090"
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3599 ø STSQLVVPEGDYLIPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSALVP
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APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQUDE TACIIIKLENFIQQKV" PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD NTSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPDESSQNRDSAPTTPTSPTEFLTPGLR SIPPLFSGKESHKSPSTKHHSPRKLKVNALPEILKEVTSVVEQAMKLPESERKKIIRR FLTTYHELIPSRKDLEMNTLYLKYSSVLLNCKVAKVFDISSFADLLSSVLPREYKTKN CAKWKDNFASESWLKNAWHFISESVSVTDDQEEPKPAFDVIVDILKDWALLPGTKFTV RLKHLLLEIGFNLVYNCDETANLYHCLVDADIPVSYVTPADVRSFLMTFSSPDTNCHI GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEESEFEVEGLPLLITLDSVLQIFDGKRPK LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYSCIHEDMKRLLPVVRA PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH GK ITDGDRLKRKQFHASVIDSVTKKRQLKDIPVQQITYTMDTEDSEGNLTTWLICNRS HARYAPGATSVSPGRMFRDLDADFRTQFSDVLDLYLGNHFKLDNCTMFRFPLRNAEMA QVSEISSVPSSDRMVQNLLDKLRSDGAELLMFLNHMEKISICEIDKATGGLNVLYSVK ENFQLCRRIISEGIWSLIREKRQEFCEKNYGKILLPDTNLLLLPAKSLCYNDCPWIKV KDSTVKYCHADIPREVAVKLGAIPKRHKALERYASNICFTALGTEFGQKEKLTSRIKS IYTAEYQDIYCLLQPILNENSHSFRGCGSYSLAVKEFLGLLKKPTYDLYINQLKQVAK SYDDGITLYQENITNACYKYLHEAYLQNEMAKATIIEKLKPFCFILVENYYVESEKVS FHLNFEAAPYLYQLPNKYKNNFRELFESYGVRQSFTYEDFALVLESIDQERGKKQITE GRFPYGSTQDYLNPIILIKLVQLGMAKDDILWDDMLERAESVAEINKSDHAAACLRSS ILLSLIDEKLKIKDPRAKDFAAKYQTIPFLPFLTKPAGFSLEWKGNSFKPETMFAATD AQKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMEC RRWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTAL EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR MTSWVEFLRNIGLKYALSQQQLLQFAKEISVRANTENWSKETLQSTVDILLHHIFQER MDLLSGNFLKELSLIPFLCPERAPAEYIRFHPQYQEVNGTLPLIKFNGAQVNPKFKQC VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALTAPAYVELLIQLKKRYFPGSDPT NQPFTEDDVRGIQNLGKGTKEGNPCKTGHYGIGFNSVYHITDCPSFISGNDILGIFDP ILNAYPSEKEMLKELLQNADDAKATEICFVFDPRQHPVDRIFDDKWAPLQGPALCVYN ELRDPLMNFVLNEKLDEFSGILRVTPCVPCSLEGHPLVLPSRLIHPEGRVAKLFDTKD DFSVICKGFYEDIAHGKGKELTRVFSDGSMWVSMKNVRFLDDSILQRKDVGSAAFKIF KEIWKTDTKGRWNTTFMRHVIVKAYLQALSVLRDLAIGGELTDYTYYAVWPDPDLVHD RRLGLVPCGAVGVLLHETQEQKWTVKPHIGEVFCYLPLRIKTGLPIHINGCFAVTSNR  ${\tt LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTVDCTTWLICTCMDTGEALKFSLNESG}$ ALNAPVLSVLKEAAKLMKTCSSSNKKLPTDVPKSSCILQITVEEFHHVFRRIADLQSP QQKRLRKFPNQFKPFIDVFGCQLPLAVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY PNTPVPIYHSRNPSKLVMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE LFKACGSIEELTSDHISMVIQKVYLKSDQELSEEESKQNLHLMLNIMRWLYSNQIPAS LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKQILLENTFSEKQFFSEVFFPNIQEIEA 9

В,

5521 TACAACAACCAGCCATTTACAGAAGATGATGTTAGAGGAATTCAGAATCTTGG 298 tacaacaaccagccatttacagaagatgatgttagaggaattcagaatcttgg 350

5573

Matches

53;

Conservative

0;

Mismatches

0;

0;

Gaps

0

Query Match Best Local Similarity

3.8%; 100.0%;

Score 53; DB 10; Pred. No. 8e-17;

Length 11493; Indels

BASE COUNT ORIGIN

RESULT 7 AC022025/c LOCUS AC022025

189760 bp

DEFINITION

Homo sapiens chromosome

10

clone RP11-489D8, complete sequence.

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RESULT
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   only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
                                                                       Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                   Tracey, A.
Direct Submission
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Human DNA sequence from clone RP11-427E4 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-DEC-2001) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
On Dec 15, 2001 this sequence version replaced gi:12957675.

Location/Qualifiers
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                                                                                                                                                                     On Feb 9, 2001 this sequence version replaced gi:11691497. During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                           Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Mammalia; Eutheria;
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/clone_lib="RPCI-11"
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Eutheria; Primates;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 bapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chf RP11-437E4 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECTOR: pBACe3.6
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  18174.
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9277. .10794
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/note="L1PA4 repeat: matches 5907. .6146 of consensus"
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/db_xref="taxon:9606"
/chromosome="6"
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                    note-"Alux
                                                                                                                           note="MSTC repeat: matches 1. .401 of consensus"
[6284. .16415
                                                                                                                                                                                               /note="MIR repeat:
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                                                               'note="AluY
                                                                                                        note-"AluJo/FRAM repeat: matches 176. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                          'note="L1MD
                                                                                                                                                                                                                                                                                                                                                                                                                   'note="L1MA8 repeat: matches 4760. .6264 of consensus"
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39028. .39154
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37243. .37
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34008. .34
                                     /note="AluJb repeat: matches 1.
43667. 43708
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                                                                                                                                                                                                                                                                                                                                                                                     /note="LIM4 repeat: matches 3889. 38640. .38678
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="33 copies 2 mer aa 66% conserved" 38342...38636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 56. .148 of consensus"
33726. .33807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31093
                                                                                                                                                                                                                                                                     /note="LIR40b repeat: matches 308. .422 of consensus" 39159. .39571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 66. .141 of consensus" 35184. .35463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2624. .2708 of consensus"
33843. .39923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER33 repeat: matches -10.
32944 .32994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="LTR33 repeat: matches 329. 32696. .32897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 13. .146 of consensus"
31943. .31984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1PA4 repeat: matches 5210. .5819 of consensus" 27848. .28190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MSTD
27238. .2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 76. .189 of consensus" 26767. .27106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MA8 repeat: matches 6183. .6250 of consensus"
25715. .25996
                                                                                                                                                                                                                                 /note="L1M4 repeat: matches 2823. .3283 of consensus"
39626. .39665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 1.
36308. .36729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="14 copies 3 mer tta 78% conserved"
32356. .32545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="27 copies 2 mer tt 72% conserved"
25620. .25714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2570. .2707 of consensus"
25307. .25360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19046. .19188
/note="MLTlJ repeat: matches 129.
                                                                                                                                 /note="LlMEc repeat: matches 1203. .1921 of consensus"
                                                                                                                                                                       /note="AluSc repeat: matches 5.
                                                                                                                                                                                                             /note="20 copies 2 mer at 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER63A repeat: matches 3. .174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1MC5 repeat: matches 7336. .7549 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat:
                                                                                             note="L2 repeat: matches 2466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note Trk33 repeat: matches 90. .141 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 76. .200 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L1MA8 repeat: matches 6250. .6285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1PA4 repeat: matches 5800. .6142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "27 copies 3 mer ata 65% conserved"
_.34082
 21 copies 2 mer tg 100% conserved'
.45177
                                                                                                                 .42147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 2229. .2695 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matches 1.
                                                                                                                                                                       .301 of consensus"
                                                         .293 of consensus"
                                                                                             .2745 of consensus"
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REFERENCE
AUTHORS
TITLE
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AC013913/c
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Best Local
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l Similarity
21; Conserv
                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insepterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2296)
                                                                                                                                                                                                                       This sequence was identified as CDM:10213920 by For further information on this sequence e-mail * NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                     Submitted (16-NOV-1999) Celera Genomics, .45 West Gude Drive
                                                                                                                                                                                                                                                                                                      Adams, M. and Venter, J.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster,
                                                                                                                                                                                                                                                                         Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                       fruit fly.
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                                                                                                                                                                       This sequence will be replaced
by the finished sequence as soon as it is
the accession number will be preserved.
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LTR16A repeat: matches 1600. .2152 of consensus"
52768. .53179
/note="LTR16A repeat: matches 25. .442 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="25 copies 2 mer ta 72% conserved"
51347 51733
/note="MLTID repeat: matches 69 .500 of
51734 52036
                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
384 c 381 g 640 t
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53672. .53886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluJo repeat: matches 1. .298 of consensus" 46349. .46454
                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53191.
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52237. .52752
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47637. .47678
/note="L2 repeat: matches 2708. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 13.
47615. .47663
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             1.5%;
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 0;
               Score 21;
Pred. No.
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Pred. No. 1.9;
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   Mismatches
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                              Length 2296
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   Indels
                                                                                                                                                                                            available and
                                                                                                                                                                                                                                         the submitter.
to fly@celera.com.
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1321 ggtatttccctggttctgatc 1341

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RESULT 1
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1332 ggttctgatccaacattatca 1352
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                                                                                                                 Local
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete
AL136322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone RP11-75C23 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RP11-75C23 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group. Further information can be http://www.sanger.ac.uk/HGP/Chr1 RP11-75C23 is from the library RPCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-JAN-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL136322.24
                                                                                                              Similarity
                                                                                                                                                                                                                                                            17559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           true right end of clone RP11-332L8 is at 2000 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tions only once, except for a short overlap.

true left end of clone RP11-53I24 is at 53955 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                 /clone="RP11-75C23"
/clone_lib="RPCI-11.1"
10247 c 10324 g 17824 t
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        /map="q31.2-32.1"
                                                                                                                                                                                                                                                                                                                                                                     /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .55954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                        1.5%; ~~
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                           Score 21;
Pred. No.
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                                                                                                              No.
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                                                                                                                 DB 9;
7.7;
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                                                                                       0,
                                                                                                                                        Length 55954;
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                                                                                 Gaps
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REFERENCE
AUTHORS
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ORGANISM
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AL445469/c
LOCUS
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence split into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fragment Name
AC091528_0
AC091528_1
AC091528_2
AC091528_3
AC091528_3
AC091528_3
AC091528_3
AC091528_3
AC091528_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21772 CTAGACAGCATCCAGTTGATA 21752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 ctagacagcatccagttgata 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  892 GGTTCTGATCCAACATTATCA 912
                                                                                                                                                                                                                      annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL445469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Dec 24, 2000 this sequence version replaced g1:11875926.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
IMPORPANT: This sequence is not the entire insert of clone RP11-254N18 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-254N18 is at 129504 in this sequence. The true right end of clone RP11-254N18 is at 129504 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats.
                                                                                                                                                                          RP11-254N18 is from the library RPCI-11.1 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA
                                                                                                                                                     http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                              VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence from clone
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200001
300001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431537
from b
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210000
310000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RP11-254N18 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AC091528 Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 110000;
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                                                                                                                                                                                                    by the group
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 107258 AATGGCCACTTTGCACTGGAT 107238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alabbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Gavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,R., Chowdhry,I., Chistopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy,Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hake,S., Hamilton,K., Harris,C., Harris,K., Hatri,M., Haylak,P., Hawes,A., Hernandez,J., Homsi,F., Howard,S., Huber,J., Hulk,S., Hume,J., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Malle,S., Martindele,A., Martindele,A., Morris,S., Moser,M., Martin,R., Martindele,A., Morris,S., Moser,M., Nickerson,B., Nwokenkwo,S., Oyuh,M., Okwuonu,G., Oragunye,N., Nickerson,B., Nwokenkwo,S., Oyuh,M., Okwuonu,G., Oragunye,N., Nickerson,B., Payton,B., Peters,L., Pickens,R., Primus,E., Pu,L., Rolfe,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157913 bp DNA linear Rattus norvegicus clone CH230-106A6, *** SEQUENCING ***, 57 unordered pieces.
                    Quiles,M., Ren.Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence. The true right end of clone RP11-118D10 is at 95065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 157913)
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/clone_lib="RPCI-11.1"
/clone_lib="RPCI-11.1"
42809. 42924
/note="Sequence from overlapping clone bAll8D10
(AL359958). Assembly confirmed by restriction digest."
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Tansey, J.,
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of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 57 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Contact: hgsc-help@bcm.tmc.edu
------Project Information
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Center clone name: CH230-106A6
------Summary Statistics
Assembly program: Phrap; version 0.990329First call to
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Direct Submission Unpublished 2 (bases 1 to 171
                                                                              Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156635:
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Pred. No.
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                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                  ACCESSION
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TITLE
                                                       AUTHORS
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1 (bases 1 to 176912)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
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                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                  AC096964
                                                                                                            Rattus
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                        Norway rat.
                                                                                                                                                                                                                                                                          AC096964.3 GI:17973319
                                                                                                                                                                                                                                                                                                                                                    Rattus
                                                                                                                                                                                                                                                                                                                                                                                   AC096964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57018 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved
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Center clone name: RP11-13403
                                                                                                                                                                                                                                                                                                           176912 bp DNA linear HTG 20-DEC-2001
us norvegicus clone CH230-202E24, *** SEQUENCING IN PROGRESS
67 unordered pieces.
6964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; L08821
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                                                                                                                                                                                                                                              HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-13403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="12q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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REFERENCE
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                                                                                         * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
be preserved.
                                               as soon as it is available and the accession number will
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Center clone name: CH230-202E24
Center clone Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 151663 bases at least Q40 Consensus quality: 160070 bases at least Q30 Consensus quality: 166999 bases at least Q20 Consensus quality: 166999 bases at least Q20 Estimated Insert size: 152238; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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COMMENT

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TITLE

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## ALIGNMENTS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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1 (bases 1 to 12793)
Hudson, T.J., Engert, J. and Richter, A.
Identification of arsacs mutations and methods of use therefor
Patent: WO 0129266-A1 26-APR-2001;
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)
Location/Qualifiers
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1650 Cedar Ave., Montreal, QC l
Location/Qualifiers
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LFKVCGSIEELTSDHISMVIORIYLKSDQDLSSPQESKQNLHLMLNII RWLYSNQIPAS
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QSSEGKMTLKKIKWPDACKERPPNYPGSIJWKGDLCNLCAPDDMCDVGHILLEIYGF ACIIIKLENFMQQKV" RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT KYSFQRFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mappling Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL157766 92693 bp DNA Human DNA sequence from clone RP11-40020 13q12.11-12.2, complete sequence.
sections only once, except for a 100
                                  IMPORTANT: This sequence is not the entire insert of clone RP11-40020 It may be shorter because we sequence overlapping.
                                                                                                                                   RP11-40020 is from the library RPCI-11.1 constructed of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 92693)
                                                                                                                                                                                                                                                                                                      database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Apr 12, 2001 this sequence version replaced gi:12709868.
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                                                                                                            //www.chori.org/bacpac/home.htm
                                                                                    pBACe3.6
              we sequence overlapping base overlap.
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true left end of clone RP11-760M1 is at 92594 in this sequence true right end of clone RP11-72P19 is at 100 in this sequence.
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                                                                                                                                                  /note="AluSq repeat: matches 1.
45261, .45312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 25871. .26011
                                                                                /note="AluY repeat: 46754 . .47052
                                                                                                                                                                                                                                                                                                     /note="AluSq repeat: matches 1.40444 .40733
                                                                                                                                                                                                                                                                                                                                                                         /note="AluSq repeat: matches 1. 39790. .40093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="THE1B repeat: 29447. .29834
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3896. .4201
                                                                                                                   45899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1ME3A repeat: matches 5787. .6164 of consensus" 36098. .36415
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                                                                                                                                                                                                                                           /note="Single clone region. Assembly confirmed by
restriction digest data."
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/clone_lib="RPCI-11.1"
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'note="L1MA10 repeat: matches 5950. .6322 of consensus"
                                                                                                                                   note="13 copies 4 mer tggt 88% conserved"
                                                                                                                                                                                                     'note="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                       /note="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                        /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluSq repeat: matches 9. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="AluSx repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 1063. .1644 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="L2 repeat: matches 2154. .2255 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2356. .2495 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg1 repeat: matches 1.
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                                 . 299
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                                                                  .298 of consensus
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65725. .66
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59350. .59
                                                                                                                                                                                                                                                                                                                      /note="AluY repeat:
                                                                                                                                                                   /note="L1PB2 repeat: 66371. .66410
                                                                                                                                                                                                                                                  65396. .65569 /note="AluY repeat: matches 5405. /55571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59992. .60223
/note="AluJo repeat: matches 85. .299 of consensus"
61036. .61144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 82. 58260. .58389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. 57331. .57390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 1685. 50704. .51032
             /note="MER31A repeat: matches 71780. .72075
                                                                                                                 /note="AluJb repeat: 69748. .69930
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Alux repeat: matches 1. .129 of consensus"
62330. .62363
/note="Alu repeat: matches 261. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="TIGGER1 repeat: matches 2238. .2418 of consensus" 62188. .62316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSq repeat: matches 129. .313 of consensus" 59992. .60223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47889. .48229
/note="AluSx repeat: matches 1.
49168. .49212
                                      /note="MER21B repeat: 71411. .71737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Alu repeat: matches
49620. .49693
                                                                                        /note="MIR repeat:
70957. .71267
                                                                                                                                                                                                                       65696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L2 repeat: matches 2581.
62008. .62187
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                                                                                                                                                                                                                                                                                                                                                             /note="TIGGER1 repeat: matches 46.
                                                                                                                                                                                                                                                                                                                                                                                      note="AluSq repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="TIGGER1 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1MB6 repeat: matches 5822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CpG island"
                                                                ALUY repeat: .71413
                                                                                                                                       10 copies 4 mer tgtg
.67886
                                                                                                                                                                                                                      .65717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '30 copies 2 mer ga
.57392
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                                                                                                                                                                                                                                  .PB2 repeat:
                                                                                                                                                                                                                                                                                                           GGER1 repeat:
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                                                                                                                                              Waterston,R.H.
Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 99819)
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                 NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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13367. .14794
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4077. .5355
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28879. .30893
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27331. .28778
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5456. .6757
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/db_xref="taxon:9606"
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Sequence 3 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 11492)
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                                         Identification of arsacs mutations and methods of use Patent: WO 0129266-A 3 26-APR-2001;

MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)

Location/Qualifiers
                                                                                                                             mouse.
        /db_xref="taxon:10090"
2280 c 2387 g 3
                         /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouchard, J.P., Mathieu, J., Melancon, S.B., Schallin Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A. ARSACS, a spastic ataxia common in northeastern Quby mutations in a new gene encoding an 11.5-kb ORF Nat. Genet. 24 (2), 120-125 (2000)
                                                                                                                                                                                                                                                                                                                              Submitted (08-OCT-1999) Genome Centre, 1650 Cedar Ave., Montreal, QC H3G 1A4,
                                                                                                                                                                                                                                                                                                                                                                   Richter, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                  Engert,J.C.,
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SSDEATIRLANMLKIEKLKTTSCLKFVLKDIGNAFYTQEEVTQLMLWILENLSSLKNE
              {	t NSNVLDWLMPLKFIHMSQGHVVAAGDLFDPDIEVLRDLFYNEEEACFPPTIFTSPDIL
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QVSEISSVPSSDRAWQNILDKLERSDGAELLMEIMHERISICEIDKATGGLINVLYSVK
QKITDGDRLKRRQFHASVIDSVTKKRQLKDIFVQQITYTMUTSVK
GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFGFLPLICKRRYFGSDFT
LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYSGIHEDMKRLLPVRA
PNIDGSDLHSAVIITMINMSTSKRTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY
RLKHLLEIGRHLVYNCDETBAHLYHCLVDADIFVSYVPPADVRSFTLMTFSSPDTWCHI
GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEESEFEVEGLPLLITLDSVLQIFDKKRKP
FLTTYHBLIFSRRDLFMNTLYLKYSSVLLNCKYKAKYPDISSFADLLSSVLPREXYKN
FLTTYHBLIFSRRDLFMNTLYLKYSSVLLNCKYKAKYPDISSFADLLSSVLPREXYKRY
CAKWKONDASESMLKNAMHFISESSVSYTDDQEEPRPAFDVIVDILLKDMALLFGTNFFTV
STSQLVVPEGDVLIFLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSALVP
LLSCHTANIDSFASILKANWHFISESSVSYTDDQEEPRPAFDVIVDILLHRIGSKDSALVP
LLSCHTANIDSFASILKANWHFISESSVSYTDDQEEPRPAFDVIVDILLHRIGSALVP
LLSCHTANIDSFASILKANWHFISESSVSYTDAKLEHLIYLKRIDSALLMY ENCNLSHLMSQDDI
KILKSLPCYKSISGRYMSIAKFGTCYVLYKSIPSAEVLEWTQSSSSAFLEEKVHLKEL
YEVLGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNILASIEEPSEIKEQLFEK
LESCLLIHDANNRLKQAAHFYDRTVRVETYMLPERMSKETIQSTVDILLHHIFQER
MDLLSGNFLKUSTALSQULQFAKRISTVRANTENNSKETIQSTVDILLHHIFQER
MDLLSGNFLKELSLIPFLCPERAPAEYIRFPQYQEVNGTLPLKFNGAQVNPKFKQC
DVLQLLMTSCPILDEKATPLSIKEQEGSDLAPQOEQLEOVNMLAUNUDDOWKLKAPEE
VVINLEYEADFKDYLYKLPLECGTFHQLFKHLGTEDIISTKQYVEVLSRIFKSSEGKQ
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VVINLEYEADFKDYLYKLPLECGTFHQLFKHLGTEDIISTKQYVEVLSRIFKSSEGKQ
LDPNEKRTQKROWSGLLENARDLALYLPSOGKLLXFEE
ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR
EGIKVSCFEKLQTTLRVGGENDIPHSRSSTFAFLKRFGRAKILSGILEBGLDE
ETPKVCQFGALCSLQGRLQCHLLSSEQFPITGLIRIMKHENDNAFLANEEKAIRLCKALR
EGIKVSCFEKLGTTLRVGGENDIPHSRSSTFAFLKRFGRAKLFLBADAGTLANGLEKAIRLDEKALLKDEL
ALAMMTIK KSATTNALISTYSLILDHAGNGTUTRT STERKLEGGLEBERLELLBADGLDE
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LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKGIVERUSSKLUDGSTLQRKDYGSAARKIF
LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKGIVERUSSKLUDGSTLQRKDYGSAARKIF
LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKGIVERUSSKLIHPEGRVAKLFDTKD
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GILGSLIDEKLKIKDPRAKDFAAKYQTIPFLPFLTKPAGFSLEWKGNSFKPETMFAATD
IYTAEYQDIVCLLQPILNENSHSFRGGGSVSLAVKEFLGLLKKPTVDLVINQLKQVAK
SVDDGITLYQENITNACYKYLHEAVLQNEMAKATIIEKLKPFCFILVENVYVESEKVS
FHLNFEAAPYLYQLPNKYKNHFRELFESVGVRQSFTVEDFALVLESIDQERGKKQITE
ENFQLCRRIISEGIWSITREKRQEFCENNYGKILLDTALCTEFGQKEKLTSBIKS
KOSTYKYCHADIPREVAVKLGAIPKHKALERVASNICFTALGTEFGQKEKLTSBIKS
ILNAYPSEKEMLKELLQNADDAKATEICFVFDPRQHPVDRIFDDKWAPLQGPALCVYN
NQPFTEDDVRGIQNIGKGTKEGNPCKTGHYGIGFNSVHITDCPSFISGNDILGIFDP b ALAMTIKSATDNLISDTSYLIAMLGONDIYRISEKLDSLGVKVDSSEBSKLELPMPGT
PIPAEIHYTILLMDPMNVFYPGEYVGYLVDAEGGDIYGSVQPTYTYAIIVQEVEREDAD
NTSFLGKIYQIDIGYSSKYKIVSSLDLYKFSREDESSQNRDSAPTTPTSFTEFLTPGLR
SIPPLFSGKESHKSPSTKHHSPRKLKVNALPEILKEVTSVVEQAWKLPESERKKIIRR
LYLKHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADKSRFTFSTSASRFQS
DKYSFORFYTSWNQEAFIKSERQQGSKEKCIPPSAGOTYSQRFFVPPTFKSVGNPVEA
RRWLRQARANFSAARNDLHKNANEWYCFKCYLSTKLALIAADYAVRGKSDKDVKFPTAL TACIIIKLENFIQQKV" TECSEMIDMRRNMDIRENLLDPGMAACHGPALWSFNNSEFSDSDFLNITRLGESLKRG EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMFDPNINHISKHIKDRSNPGIKINWSK LVESVHVNLEQALSIETKPTINAVLKHEKTVVDWYTSKTESDBDYQGGOHILLEIYGF MHDHLSEGKDSFKALKFPWWTGKNFCPLAQAVIKPTHDLDLQPYLYNVPKTMAKFHQ LFKACGSIEBLTSDHISMVIQKVYLKSDQELSBEBSKONLHLMLNIMRHLYSNQIPAS PNTPVPIYHSRNPSKLVMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE AQKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMEC HARYAPGATSVSPGRMFRDLDADFRTQFSDVLDLYLGNHFKLDNCTMFRFPLRNAEMA RRLGLVPCGAVGVLLHETQEQKWTVKPHIGEVFCYLPLRIKTGLPIHINGCFAVTSNR LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTVDCTTWLICTCMDTGEALKFSLNESG ALNAPVLSVLKEAAKLMKTCSSSNKKLPTDVPKSSCILQITVEEFHHVFRRIADLQSP NTADIYSLYDEFSLCGHRLIIFTQSYNSMYLKYLKIEETNPSLAQDTIIIKKKYCPSK QQKRLRKFPNQFKPFIDVFGCQLPLAVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY 2281 c g

밁 Q Q Query Match Best Local S Matches 1266 Local Similarity 90.: hes 1266; Conservative 83.8%; 0; Score 1174; DB 10; Pred. No. 8.8e-265; 0; Mismatches 135; Indels Length 11493; 1; Gaps 120

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CCTCTCTCTTTGGAGACAGGGCTGCCATTTCATGTGAATGGCCACTTTGCTCTAGATTCA
           cctctttctttggagactgggctgccatttcatgtgaatggccactttgcactggattca
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                                                                                                                                                                                                      product or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/sservices/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi.bin/sp.cgi).
                                                                                                                                                                                                                                                                                                                                                                                 Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please so
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-MYJ24
Genes with similarity to proteins in the databases are described
'product' or 'note' qualifiers. Genes that have no significant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-AUG-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Arab
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AB006708.1 GI:23
                                                                                                                                   http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 78844)
                                                                         r because we remove overlaps between clone is T2007 and the 3' clone is M Location/Qualifiers
/organism="Arabidopsis/strain="Columbia"
/db_xref="taxon:3702"
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genomic
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                                                                                                 neighboring MKD15.
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me 5, P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mosome 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis
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न by
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CDS
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AYLNPARNCLINGFKRRELDDIYURMOEGSDDLPVNWTLLELSOVMLAHALSALG
LEEESAIAVDMPMNVESVIIYLAIVLAGHVVVSIADSFSPREISTRLKISKAKAIFTO
DVIIRDKSIPLYRRVDAEAPLAIVVPARGSSCRMKLEKEDLSWNNFLGNARNLRGV
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ORGDVVAWPTNLGWMMGPWLVYASLINGACMGLYNGSPLGPTFAKFVODAEVSVLGVI
PSIVREWONSNSTSGVDWSRIRCFGSTGEASNIDEYJMLMGRAHYKPVIGYGGTEIG
GSFIGSSLAOPOSLAAFSTAAMGCKLETILDEDSNPIPDYAAGVGELALCPHMGGASST
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IERVCNSVDDSYLETAAIGVPPPSGGFBQLVIAVVFKSBEFSNPDLNLLKKSFNSEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGSLIIPMIPTELIQPTWTLELLTSLVAYVFLFLSCTFLK"
complement()0in(21486. .21596,21673. .21885,21982. .22080,22156. .22281,22380. .22596,23171. .23391,23446. .23549,23686. .23811,23899. .23939,24271. .24475,24564. .24820,24909. .25038,25122. .25183))
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LFLFAFMGGWSIMNSAEGGPAFQVAVSLAACVYFLNEKTKSLGRACLIGIGALVAGWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALSGRGIGNVKTGDYQNWIGNHFLRGKNWEGITKCLSDSRVCKRFGPRDIDFDSKHL SNVQEGCCRPPVECGFESKNATWWTVPATATTAIIGDCKAWSNTORQLCYACESCKIG VLKGIRKRWRILIVVHLLLILVVFLYSCGCCVRKNNRVPWKRRFF COMPLEMENT (Join (19438. .19588, 19681. .19757, 19838. .20220, 20533. .20633, 20839. .20903))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="senescence-associated protein 5-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFVSCCSAESKKVATSATDLKPIMERRPEYIPKKLPHKNYVRYLDTTLEDGEOSPGAA
LTPPOKLEIAROLAKLRYDLMEVGFPVSSEEBEFAIKTIAKTVGNEVDEETGYVPVIC
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VIENTPGADDIVFAIHCHNDLGVATANTISGICAGAROVEVTINGIGERSGNAFLEEV
VMALKCRGESLMDGYYTKIDSRQIMATSKMYQEHTGMYVQPHKPIVGDNCFYHESGIH
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11261. .11335,11485. .11607)

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COMplement()oin(26733...26967,27047...27178,27258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDGILKNRSTYEILSPEDVGIVKSENSGIVLGKLSGRHAVKDRLKELGYEISDEKFND IFSRYRELTKDKKRITDADLKALVVNGAEISSEKLNSKGINDLMSSPQISAVV" join(16792. .17283,17380. .17682)
                                            gene_id:MYJ24.5
similar to unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="2-isopropylmalate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MASLLLTSSSMITTSCRSMVLRSGLPIGSSFPSLRLTRPYDKAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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.10955,11061. .11094,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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GGGDKTKTTTTAAVSRRLVEEPMWRTYCNGKKCGFATRRECGEKEKKVLKALEMVSMG
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Dr1 protein homolog"
                                                                                                                                                                                                                                                                                                              similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                         43530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECCVEFINLVSSESNDVCNKEDKRTIAPEHVLKALQVLGFGEYIEEVYAAYEQHKYET
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FFGDLYEFCREAADKEGKTVÍVAGLDGDFMRRRFGSVLDLIPIADTVTKLTSRCEVCG
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KPALDTALPIAKQAGEEAMKLASPAFSEASKKAQEAMQSSGFDSEPVFNAAKTVTDVA
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unknown protein"
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IVRNSKRVEAEIAALKISYLKKINKGSNIIILDSYTDSAKIVAKTLKVLGYKNCYIVT
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7. .36652,36881. .37020,37165. .37233,37356. .37417,
8. .37601,37818. .37912,37989. .38079,38728. .38862))
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    .39912,40006. .40176)
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Matches

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593 attttaaactggataat 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGTGACTTGGAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgtatcatatcacagactgcccatcttttatttctggcaatgacatcctgtgtatttttg 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCAAGCAAACTTGAAAAACCTTTTGCAATAGGAAGATTTGGGCTGGGATTTAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaggcacgaaagagggaaatccttataaaactggacagtatggaataggattcaattctg 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtgtgtacaaccagccatttacagaagatgatgttagaggaattcagaatcttggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agcatccagitgatagatatitgatgataagtgggccccattgcaagggccagcactit 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccagcagaattaagagcatccttaatgcatatccttctgaaaaggaaatgttgaaagagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGCTGGAAGATATATATTGGACCAGTTTCCTGATCAATTTTGCACCATTCTTGCATTTTTG 53422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCTCATGCCAATCATTTGCCTGGTATTTCTCCAACTCACCCAGGGTTGCGGATTAAAT 53362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATGGGACGTCTTCACTCCTATCTCCTGAAATGGCAGATTGGCAAGGCCCTGCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTTCAAAATGCGGAAGATGCAGGAGCTTCTGAGGTGACATTCCTTTTGGATAAGACTC
                                                                                                           Tu,Y.F., Jia,J., Yin, H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H., Tu,Y.F., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H., Chen,X.Y., Shao,C.Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,W., Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L., Zhu,F.H., Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q.J., Zhang,L., Lu,Y.L., Wu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J., Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T., Zhang,Y.J., Lu,Y., Zhang,Y.J., Hu,H., Jia,P.Y., Jian,Y.M., Ying,K., Jian,J.M., Jian,J.M., Ying,K., Jian,J.M., Jian,J.M., Jian,J.M., Ying,K., Jian,J.M., 
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 165299)
      Submitted (28-JUL-2000) Han
                                     Direct Submission
                                                                     and Hong, G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa chromosome 4 clone OSJNBa0018M05,
                                                                                              Zhou, B., Chen, Z.H., Hao, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:15552695
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Pred. No. 1.4e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165299 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
Bin,
                                                                                        Zhang, L.,
      National Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259;
                                                                                           Wu, M., Zhang, R.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
M05, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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      for
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      Gene
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                                                                                              Guan, J.P.
   Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
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                                                                                              AC069017
                                  leces
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KEYWORDS SOURCE

ORGANISM

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RESULT 8 OSJN00002/c

DEFINITION ACCESSION

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38846 CAATGAATTTGAGTTTGTCAGGGGTTGCTGAGGCTTTTGGACAGCATGAAGATTTGACTA 38787
                                                                                                                                                                                                                                                                                                                                                                                                                                            38546 ACAGCAAACTTGAGAAACCTTTTGCAATAGGCAGGTTTGGTCTTGGCTTCAATTGTGTAT
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                                                                                                                                                                                                                                                                                                                                                38486 ATCACTTCACAGACATTCCTGGGTTTGTTTCTGG----TGAGAATATTGTTATGTTTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gcacgaaagagggaaatccttataaaactggacagtatggaataggattccaattctgtgt 415
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                                                                                                                                                   TAGGAAGGAGCATCTTAGAACAGTTCCCTGAT 38338
                                                                                                                                                                                            tggatgcagattttaggacacagttctcagat 567
                                                                                                                                                                                                                                                  CGCATGCCTCTTATCTGCCAGGAATATCTCCATCTCATCCAGGTCTAAGGATAAAATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgtacaaccagccatttacagaagatgatgttagaggaattcagaatcttggaaaag 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinese Academy of sciences, 500# Cao Bao Road, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the finished sequence as soon as it accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="OSJNBa0018M05"
/clone_lib="CUGI-OSJNBa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /variety="Nipponbare"
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174140 bp
MGS3-342I16,
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Pred. No. 5.8e-17;
0; Mismatches 238;
DNA linear HTG
WORKING DRAFT SEQUENCE,
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-kocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 12, 2001 this sequence version replaced gi:14787161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer Bodipy: 37% of reads
Chemistry: Dye-terminator Big Dye: 63% of reads
Chemistry: Dye-terminator Big Dye: 63% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 17525 bases at least Q40
Consensus quality: 179254 bases at least Q30
Consensus quality: 181014 bases at least Q30
Consensus quality: 178322; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.4x in Q20 bases; sum-of-contigs estimation
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87026
136729
136829
159943
160043
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/organism="Mus musculus"
                                                                Location/Qualifiers
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                                                                                      86925: contig of 86925 bp in length 87025: gap of unknown length 136728: contig of 49703 bp in length 136828: gap of unknown length 159942: contig of 23114 bp in length 160042: gap of unknown length 168814: contig of 8772 bp in length 168914: gap of unknown length 174140: contig of 5726 bp in length
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PFMAL13P3/c
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                                                                                                                                                                                                                                                      phage etc.
Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* This record will be available and the accession number will
                                                                                                                                                                                                                                                                                                                                                           on Aug 24, 1999 this sequence version replaced gi:5731882. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB10 1SA, U
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Plasmodium falciparum chromosome 13
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Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Barrell,B.
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/clone="MGS3-342I16"
32907 c 34252 g 55
                                                                                                                     /db_xref="taxon:5833"
/chromosome="13"
                                                                                                                                                          /organism="Plasmodium falciparum"
/strain="3D7"
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                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                           Submitted (13-MAY-1999) Anatomy University, 630 W 168 Street, N
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                                                                                                         Direct Submission
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/db_xref="taxon:44689"
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                                                                                                                                                                                                                                                                                                                           1823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             694 gtccagaatcttttggacaaactgcgctcagatggggcagaacttctaatgtttcttaat 753
                                                                                                                                                                                                                                                                                  <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                  tctgtaattgatagtgttactaaaaagaggcagctcaaagacataccagttcaaccaaata 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                              tattcagtaaagggcaaaatcacagatggagacagattgaaaaggaaacaatttcatgca 873
                                                                                                                                                                                                                                                                                                                                                      accta 938
                                                                                                                                                                                                                                                                                                                                                                                 AATATAATTGAAGAAGAAATTGAACAAGAGGAGGAAAATATTGAAAAAAGATCAACAACAA 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTCGAAAATTTTGCTGATATACTTTTAGATGAAGGTAATAAAGATGGAAATGTAGTT 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cacatggaaaaaatttctatttgtgaaatagataagagtactggagctctaaatgtgctg 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCAACATCATTGTGGTGATGTTGGTTCTCATATTGGTACTCCTCAAGTCTATAATGCA 1642
                                                                                                                                                                                                                                                                                                                           ACCCA 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                          120;
                                                      Nelson,M.K., Clark,A., Abe,T., Nomura,A., Yadava,N., Funair,C.J., Jermyn,K.A., Mohanty,S., Firtel,R.A. and Williams,J.G.
An F-Box/WD40 repeat-containing protein important for Dictyostelium cell-type proportioning, slug behaviour, and culmination Dev. Biol. 224 (1), 42-59 (2000)
                                                                                                                                                            Dictyostelium discoideum
                                                                                                                                                                                                                      Dictyostelium discoideum F-Box A protein (fbxA) gene, AF151733
 Nelson, M.K.,
                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                          Dictyostelium discoideum.
                                                                                                                                                                                                        AF151733.1
                                                                                                                                                                                                                                                   AF151733
                              10898960
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(bases 1 to 3885) son, M.K., Clark, A.,
                                                                                                                               (bases 1 to 3885)
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/allele="A"
230. .>2389
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/protein_id="AAD37800.1"
/db_xref="GI:5007064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFHKKTPKRKQIIHSNLSNDENKVNSNSGDSADGSSSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTYYFSNSGFDNLPEEVVQIIFSNLSAINIVNLSLVCKRFKMATDSPILWKNLYKSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start-]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="2"
                                                                                                                                                                                                        GI:5163417
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Pred. No. 2.9;
0; Mismatches 125;
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Abe, T.,
                                                                                                                                                                                                                                                  3885 bp
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Nomura, A., Firtel, R.A.
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3.9;
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                                          934 accta 938
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nes 120; Conserv
                                                                                                                                                                                                                                                  GTTCAACATCATTGTGGTGATGTTGGTTCTCATATTGGTACTCCTCAAGTCTATAATGCA 1554
                                                                                               tctgtaattgatagtgttactaaaaagaggcagctcaaagacataccagttcaacaaata
                                                                                                                               tattcagtaaagggcaaaatcacagatggagacagattgaaaaggaaacaatttcatgca
                                                                                                                                                                                        ATGGTCGAAAATTTTGCTGATATACTTTTAGATGAAGGTAATAAAGATGGAAATGTAGTT 1614
                                                                                                                                                                                                       cacatggaaaaaatttctattgtgaaatagataagagtactggagctctaaatgtgctg 813
               ACCCA
                                                                       AATATAATTGATGAAGAAATTGAACAAGAGGAGGAAAATATTGAAAAAGATCAACAACAA
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1739

933

873

Conservative

3.2%;

; Score 45; DB; ; Pred. No. 2.7; 0; Mismatches

ω •• 125;

Length 3885; Indels

0;

Gaps

0

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Submitted (14-MAY-1999) Biology,
Street, Meadville, PA 16335, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, J.G.
Direct Submission
  a
MWRNTITMRLLQSVKKGPGNFSSVHWRSICSPNYQVADGIEVHYLPTALLNYGLGDGS
FTSFLAAIEVKGYPTPWEEEMVTKMFAARIISNQNSIINHVNKLTGGSEMIRELPVIP
SVQHHCGDVGSHIGTPQVYNAMVENFADILLDEGNKDGNVVSSKNKRKRNKNNENKNN
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SSHERGIYLSKGVAEENISPENNYELLLDISSRSKWDFFGCREAHIIEVDHLHHIHL
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QKDKCKMTFVQQCDLRDIELQRIPGYKSFNSKERLEDBQFLTLEPATVSGRLAKIFES
IELYISNNVMDIETKDIRISIMEKAEKEVNEMFGTTNPDYGWKIYLKKLDMEILIKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD40673.1"
/b_xref="GI:5163418"
/transla++--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="fbxA"
join(1. .237,379. .3885)
/gene="fbxA"
                                                                                                                                                                                                                                                                                                                                                                                                     TSGYYMIGKGSFSSRYSPELLADVLYQKNPFEWDTFYDKTKLVESINSSIREVEVHYR
                                                                        DYMALTGSTDKTLKLWDLRQASTFISSYSTKHTGPIRCISYQEKNGIVLSGSDDGSII
                                                                                              TKKITQSKIVAQHELSNKGIVFTTSSDKSAKVWDLTNGTCINTLVGHSYAVNCIEPIG
                                                                                                                    MVDFIEQPIEVIHTSRPTNLADGFDFTFPGKYLIWEHTIIHYWDVETSTLLWNELNAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="position 6110"
join(<1. .237,379. .>3885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="regulate cell fate"
/note="FbxA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="F-Box A protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="fbxA"
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/chromosome="2"
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium amoebae lacking an F-box protein form spores rather than stalk in chimeras with wild type Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3292-3297 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DICTYSTELLUM discoideum cheater ChtA (cht) gene, cht-A allele,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-1999) Anatomy and Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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Ennis, H.L., Dao, D.N., Pukatzki, S.U. and Kessin, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dao, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F-box protein is essential for development in Dictyostelium
                         1559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ennis, H.L., Franke, J., Kessin, R.H., Nelson, M.K. and
                                                                                                                                                                                                                                                                                                                                SSHERGIYLSKGVAEFNISPENMYELLLDISSRSKWDFHCREAHIIEEYDHLNHIHL
METNPLISNLDMNLYRSCKYDPQERLEVIAMRSIELEDGDVDQFECLENGWVIQGLRG
QKDKCKMFFVQQCDLRDIELQRIPGYKSFNSKERLEDPGFLIFPAFVSGRILAKIFES
IELYISNNVKDIETKDIRISIMEKAEKEVNEMFGTTNPDYGWKIYLKKLDMEILIKKT
TSGYYMIGKGSFSSRYSPELLADVLYQKNPFFWDTFVDKTKLVESINSSIREVEVYYR
MWRNTITMRLLOSVKKGPGNFSSVHWRSICSPNQVADGIEVHYLPTALLNYGLGDGS
ETSFLAAIEVKGYFTPWEEEMVTKMFAARIISNQNSIINHVNKLTGGSSMIRELEPVIP
SQVHHGGDVGSHIGTPQVYNAMVENFADILLDEGNKDGNVVSKNKRKRNKNRENKNN
                                                                                                                                                                                             TEKKIKFWNLNTGQCIGDYEGESGVLSVEYDHTQKSSCIWPLSDYTKVHIGHKNGTVT
MVDFIEQPIEVIHTSRPTNLADGFDFTFPGKYLIWEHTIIHYWDVETSTLLWYELNAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y, 630 W 168 Street, New York, NY 10032, USA Location/Qualifiers
                                                                                        DYMALTGSTDKTLKLWDLRQASTFISSYSTKHTGPIRCISYQEKNGIYLSGSDDGSII
                                                                                                             TKKITQSKIVAQHELSNKGIVFTTSSDKSAKVWDLINGTCINTLVGHSYAVNCIEPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="cht"
/allele="A"
                                                                                                                                                                               NSYIPDEEFINWKSHYTEKHKQSKRWVNMEPIRITPLKGHNRAIKAVKSEGNSAITVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MQYVNGNDISSQSIHEVLELAFSTKIPWTKLEYESSEKHIIHSY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAD37799.1"
/db_xref="GI:5007062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="cheater ChtA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostelium discoideum"/strain="AX3K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="f-box protein with WD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="cht"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="cheater ChtA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="cht"
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/chromosome="2"
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REFERENCE
AUTHORS
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KEYWORDS
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HS425C14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1735 ACCCA 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1495 GTTCAACATCATTGTGGTGATGTTGGTTCTCATATTGGTACTCCTCAAGTCTATAATGCA 1554
                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1555 ATGGTCGAAAATTTTGCTGATATACTTTTAGATGAAAGGTAATAAAGATGGAAATGTAGTT 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          814 tattcagtaaagggcaaaatcacagatggagacagattgaaaaggaaacaatttcatgca 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694 gtccagaatcttttggacaaactgcgctcagatggggcagaacttctaatgtttcttaat 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        934 accta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874 tctgtaattgatagtgttactaaaaagaggcagctcaaagacataccagttcaacaaata 933
                                                                                                                                                                                                                                          Clone requests: clonerequest@sanger.ac.uk
On Jul 1, 1998 this sequence version replaced gi:3250834.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above. This sequence is the
entire insert of clone 425C14. This sequence has been finished
according to sequence map criteria as follows. An attempt is made
to resolve all sequenceing problems, such as compressions and
repeats, but not necessarily within known annotated human repeat
sequence elements (e.g. Alu). Where the sequence is ambiguous,
there is an annotation using the 'unsure' feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacatggaaaaaatttctatttgtgaaatagataagagtactggagctctaaatgtgctg 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
299129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS425C14 160203 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete
                                                                                                           425C14 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                               Mapping Group. Further information can be http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-JUL-1998) E-mail enquires: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mashreghi-Mohammadi,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 160203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                         1. .160203
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:3281967
33; Heat Shock Transcription Factor; HSF2; HSTF2.
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                                                                 region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HSF2",
join(<9584. .9692,9848. .9975,10736. .10860,13432. .13507,
16379. .16440,17346. .17433,19361. .19509,19929. .20168,
20792. .20897,25114. .25167,28641. .28725,29136. .29431)
/gene="HSF2"
                                                                                                                                              /note="MIR repeat: matches 71..251 of consensus" 12944..13243 /note="AluSx repeat: matches 2..292 of consensus" complement[14421..14487)
                                                                                                                                                                                                                                                                               complement(11178..11670)
/note="match: GSS B51948"
complement(11840..12127)
                                                                                                                                                                                                                                                                                                                                          SIDCSLEDFQAMLSGROFSIDPDLLYDLFTSSVQMNPTDYINNTKSENKGLETTKNNV
VQPVSEEGRKSKSKPDKQLIQYTAFPLLAFLDGNPASSVEQASTTASSEVLSSVDKPI
EVDELLDSSLDPEPTSSKLVRLEPLTEAEASEATLFYLCELAPAPLDSDMPLLDS"
                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MGGSFLYLDEQRFAKEILPKYFKHNMAASFVRQLNMYGFRKVVHIDSGIVKQERDGPVEFQHPYFKQGQDDLLENIKRKVSSSKPEENKIRQEDLTKIISSA QKVQIKQETIESRLSELKSENESLMKEVSESHAKHAQQQQVIRKIVQFIVTLVQNNQL VSLKRKRRLHINDAKKKNLFQHIVKEPTDNHHHKVPHSRTEGELKPRERISDDIIV DVTDDNADEENIPVIPETNEDVISDPSNCSQYPDIVIVEDDNEDEXAPVIQSGEQNEP ARESLSSGSDGSSPLMSSAVQLNGSSSLTSEDPVTMMDSILNDNINLLGKVELLDYLD ARESLSSGSDGSSPLMSSAVQLNGSSSLTSEDPVTMMDSILNDNINLLGKVELLDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="dJ425C14.1 (Heat Shock Factor 2 (HSF2,
/product="dJ425C14.1 (Heat Shock Factor 2))"
/shock Transcription Factor 2, HSTF 2))"
/protein_id="CAB16203.1"
/db_xref="GI:3294179"
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/clone_lib="RPCI-3"
complement(1...61)
                                 /note="MER5A repeat: matches 189.
complement(15855. .15982)
/note="FLAM_C repeat: matches 128.
                                                                                                     /note="MER5B repeat: matches 74. .7 of consensus"
complement(15495. .15671)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4425. .4846)
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/note="FLAM_A repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS AQ013878"
2351. .2483
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                                                                                                                                                                                                                                        /note="AluSx repeat: matches 300. .1 of consensus"
12541. .12723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Aluyb8 repeat: matches
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tches 302
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/gene="HSF2"
/note="match: STS G13562"
complement(29857. .30169)
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/note="MIR repeat: matches 49. .
complement(26830. .27596)
/note="L1 repeat: matches 4031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38566. .39641
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38261. .38558
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/note="MSTB r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="dJ425C14.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1.
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/note="LIMD1 repeat: matches 749. .390 of consensus" complement(join(40559. .42390,43985. .44215,44332. .44476,4875. .48965,49099. .49268,50981. .51118,51362. .51441,53692. .53861,55731. .>58892))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: STS G24632"
34383. .34412
/note="15 copies 2 mer tg 93% conserved"
35013. .35126
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complement(32572...32874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1 repeat: matches 3943. .5041 of consensus"
complement(39724. .40048)
/product="dJ425C14.2 (Placental protein DIFF33 LIKE)"
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                                                          5564 AAGGCTTTTTTTTTTTTTTATGGAACTTGATTTTAAAACATATGTGGAAGAGCTAAAGAC 5506
                                                                                                                              5684 AACATAAATCAACAAAATGAATTTAGAAATATGCCTTGTCATGAGAATACACAACACAGA 5625
                                                                                                                                                                                               5744 TACAACATATAAGATATCCAGGAAGAAAATGAACAAAGATCCACAAGGCCTAATAGCA 5685
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               496 ggggccacatccattagtcccggacgcatgtttagagattttggatgcagattttaggac 554
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Search completed: May 22, 2002, 06:53:41 Job time: 8806 sec

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## ALIGNMENTS

RESULT AAH20176 autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; Synthetic abnormal neuronal lipid storage; genetic disorder; characterisation; ds Human mutated spastin nucleotide sequence SEQ ID NO:7. 09-AUG-2001 AAH20176; AAH20176 standard; 20-OCT-1999; 20-OCT-2000; 2000WO-US29130 26-APR-2001. WO200129266-A2 Homo sapiens. Human; mouse; spastin; ARSACS; chromosome 13q11; identification; ب (first 99US-0160588 Location/Qualifiers 77..6604 /\*tag= a /product= "mutated spastin" DNA; entry) 12792 ВP

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cc gene therapy and as a spastin polypeptide agonists. (1), their fragments cor their complements can be useful for assaying the presence of a nucleic carid molecule in a sample. (1) is useful for diagnosing or aiding in the cc diagnosis of an early onset neurodegenerative disease in an individual. Cf the neurodegenerative disease reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, ct atrophy of upper cerebellar vermis, absence of Purkinje cells and cannormal neuronal lipid storage. (1) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome can arkers, to identify genetic disorders, as hybridisation probes or curies an antigen, identify and express recombinant protein for canalysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disorder associated with aberrant expression cr activity of (1). The assays can be utilised to identify a subject or notein or spatin can easien or activity the present contacts of the present protein or activity of the present protein or activity of the present protein protein or activity of the present protein the protein or activity of the present protein or activity of the present protein or activity of the present protein the protein or activity of the present protein or activity of the present protein the protein or activity of the present protein or activity the protein to contact protein the protein or activity of the present protein or activity of the present protein or activity of the protein the protein to the protein or activity of the protein the protein the protein or activity of the protein the 
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N.B. The present sequence is not given in the is derived from the human spasiin nucleotide s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide, encoding spastin gene, and polynuseful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations
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The present invention describes human and mouse spastin, and mutated CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in GC gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic correct of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease comprises reduced sensory nerve conduction, cc reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC analysis, characterisation or therapeutic use, or as markers for tissues CC in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression crecion or spastin gene expression or activity. The present sequence encodes human spastin as given in the present invention.
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
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                                                     New isolated polynucleotide, encoding spastin gene, and puseful for diagnosing autosomal recessive spastic ataxia Charlevoix-Saguenay disease by detecting two point mutat:
                                                                                                                                                                                                                                                                                                            Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
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(C (ARSACS)) gene sequences (I). The spastin gene has been mapped to C chromosome 13q11. (I) have neuroprotective activities and can be used in C gene therapy and as a spastin polypeptide agonists. (I), their fragments C or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the C diagnosis of an early onset neurodegenerative disease in an individual. C reduced motor nerve velocity, hypermyelination of retinal nerve fibres, catrophy of upper cerebellar vermis, absence of purkinje cells and C abnormal neuronal lipid storage. (I) can also be used to produce C antisense nucleic acids, is useful as molecular weight or chromosome C markers, to identify genetic disorders, as hybridisation probes or C primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from C the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with abarrant expression or arctivity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin
                                                                                 protein or spastin gene expression or activity. The present sequence represents a mutated human spastin gene from the present invention. N.B. The present sequence is not given in the present secilication is derived from the human spastin nucleotide sequence (AAH20174) as
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Sequence 12793 BP; 4163 A; 2255 Ç; 2487 <u>ი</u> 3888 ₽. 0 other

Query Match
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Similarity 99.9 01; Conservative

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CC human spastin (autosomal recessive spastic staxia of Charlevolx. Sadyenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in CC gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC diagnosis of an early onset neurodegenerative disease in an individual. (CC The neurodegenerative disease reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and CC antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC markers, to identify genetic disorders, as hybridisation probes or CC markers, to identify genetic disorders, as hybridisation protein for CC markers, to identify genetic use, or as markers for tissues in which the corresponding protein is expressed. Disgnostic methods from CC the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or spastin gene expression or activity. The present sequence encodes a mutated human spastin
                           N.B. The present sequence is derived from the human stated on page 14.
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The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purking cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or
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N.B. The present sequence is not given in the present specification but is derived from the human spastin nucleotide sequence (AAH20174) as stated on page 14.
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                                                                                                                                                                                                                                                                                                                                                   9tagcagtaaaactaggagcagtcccaaagcgacacaaagccttagaaagatatgcatcc
                 | aacaaccagccatttacagaagatgatgttagaggaattcagaatcttggaaaaggcacg
                                                                              gttgatagaatatttgatgataagtgggccccattgcaagggccagcactttgtgtgtac
                                                                                                                                                aatgctgatgcaaaggcgacagaaatctgttttgtgtttgatcctagacagcatcca
                                                                                                                                                                                                                  attaagagcatccttaatgcatatccttctgaaaaggaaatgttgaaagagcttcttcaa
                                                                                                                                                                                                                                                                                 gtagctgtaaaacttggtgcaataccaaagagacataaagcattagaaagatatgcatcc
                                                                                                                                aatgctgatgatgcaaaggccacagagatctgctttgtgtttgatcctagacagcatcct
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Pred. No. 0;
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             gtaaaggacactttaaagaagt
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                                                                                                                                                                                                                                                                                    ggagtagcagcctgcattactcacaattataaaaagccccacagagccttctgctttctg
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                                                                  cggtatttccctggttctgatccaacattatcagtgttacagaacacccctattcatgtt
                                                                                                                                                                      gccagaagaaacttg
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RESULT 7
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Best Local :
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                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                   4896
                                                                                                                          4956
                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antitheumatic; antiarthritic; antidiabetic; antipsoriatic;
  4776 CAAACAAAATAAAACTAATAATTTTA 4750
                                                                                                                                                                                                                    Sequence 7990
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 131; 32pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated
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                     914
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                                                                                                                                         734 aacttctaatgtttcttaatcacatggaaaaaatttctatttgtgaaatagataagagta
                                                                                             ctggagctctaeatgtgctgtattcagtaaagggcaaaaatcacagatggagacagattga
                    acataccagttcaacaaataacctata
                                                   aaaggaaacaatttcatgcatctgtaattgatagtgttactaaaaagaggcagctcaaag
                                                                                                                         AACAACAAACTTTTATTATAAAAAACTAACAAATTATCCACTTATAACATAAAAATAACTA
                                                                                CACGACCGCTAAAAAAACATTCTAATTCTAAATACTAAAATTCGACATTACCACATCATTC
                                        immune system disease; cytosine methylation;
                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock
                                                                                                                                                                  Conservative
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2000DE-1043826
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Pred. No. 0
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Query Match
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                 1361
                                                                                                                                                              1241 ttcgaagtgactggaattaacagtttaatgacagcattaatagctcctgcatatgtgaatt 1300
                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
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                                                                                                                                                                                                                                                                                                Sequence 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human foetal liver single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 8085; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-)
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387
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                               gaacacccctattcatgttgtaaaggacactttaaaga
                                                                                             gctaatacagttaaaaaaacggtatttccctggttctgatccaacattatcagtgttaca 1360
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GAAAAAAGTAAATCATCCTGAAGTTAAGTCTTTAATGA
                                                                     TTTCATAGAGACAGAGTCTCACTATGTTTCCCAGTCCTAATAAACATTATGTGATAAAAA
                                                                                                                                       foetal liver;
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2000US-0236359.
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2000US-0608408.
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derifrom the human heart via microarrays. By measuring gene expression, probes are useful for predicting, disgnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular seg. cardiovascular disease, hypertension, cardiac arrhythmias and
                    1361
                                                           1301
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                                                                                                                                                                        Sequence 531
                                                                                                                                                                                                                                                                                                                             Claim
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26-MAY-2000;
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                                                                                                                                                                                                                          congenital heart disease.
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                                        447
  387
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                                                                                          ttcgaagtgactggaataacagtttaatgacagcattàatagctcctgcatatgtgaatt 1300
GAAAAAAGTAAATCATCCTGAAGTTAAGTCTTTAATGA
                  gaacacccctattcatgttgtaaaggacactttaaaga
                                                         gctaatacagttaaaaaaacggtatttccctggttctgatccaacattatcagtgttaca
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed emicroarray; Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    esent invention provides a number of single exon nucleic which are derived from genomic sequences expressed in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression analysi
nultiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
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                                                                                                                                                                                                                                                                                                                                                                                                                      .51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                   74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              531;
                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 12
AA11573/C
ID AA1165
XX
AC AA1165
XX
DT 12-OCT
XX
XX
XX
Probe
XX
VW Probe;
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                  1361
                                                                                                                                                                                                                                           1241 ttcgaagtgactggaataacagtttaatgacagcattaatagctcctgcatatgtgaatt 1300
                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon;
 Probe; human; microarray;
                       Probe #6506
                                             12-OCT-2001
                                                                                                                                                                                                                                                                                                                                Sequence 531 BP; 156 A; 108 C; 107 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
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                                                                  AAI16573;
                                                                                       AAI16573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                       447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                             387
                                                                                                                                                                                                                                 507
                                                                                                                                                           gaacacccctattcatgttgtaaaggacactttaaaga 1398
                                                                                                                                            GAAAAAAGTAAATCATCCTGAAGTTAAGTCTTTAATGA
                                                                                                                                                                                                         gctaatacagttaaaaaaacggtatttccctggttctgatccaacattatcagtgttaca 1360
                                                                                                                                                                                                                                2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                      TTTCATAGAGACAGAGTCTCACTATGTTTCCCCAGTCCTAATAAACATTATGTGATAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone marrow expressed
                                                                                                                                                                                                                                                                                    Similarity
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                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                     for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:
                                                                                       DNA;
                                                                                                                                                                                                                                                                                   2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 8482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                                       531
 gene expression;
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                                                                                                                                                                                                                                                                                    Score 39.6; DB Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphoma;
                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR,
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Listing;
                                                                                                                                                                                                                                                                                                                                160 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myeloma;
cervical epithelial cell;
                                                                                                                                             350
                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                          74;
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is one of
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RESULT 13
AA139650/c
ID AA1396
XX AA1396
XX IT-OCT
XX Probe
XX Probe;
XX Pro
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                        1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs, can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
                       genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1301
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                                            Probe; microarray; human;
                                                                                            Probe
                                                                                                                                    17-OCT-2001
                                                                                                                                                                                   AAI39650
                                                                                                                                                                                                                              AAI39650 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                             387
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                                                                                                                                                                                                                                                                                                                                                                                   gaacacccctattcatgttgtaaaggacactttaaaga
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                                                                                                                                                                                                                                                                                                                                             GAAAAAGTAAATCATCCTGAAGTTAAGTCTTTAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCATAGAGACAGAGTCTCACTATGTTTCCCAGTCCTAATAAACATTATGTGATAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single (
                                                                                         #8336 used to
                       disorder;
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2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-02346359.

2000US-0236359.
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                                                                                                                                    (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 A;
                                                                                                                                                                                                                                DNA;
                                                                                       measure gene
                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 C;
                                                                                                                                                                                                                                531
                                            placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z,
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                                                                                                                                                                                                                                ВP
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human cervical epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 G; 160
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                                                                                       expression
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                                               antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                        1398
                                                                                         in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
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RESULT 14
AAK8759/C
ID AAK875
XX AAK875
XX O7-NOV
DT 07-NOV
XX Human
XX Human
XX Human
XX Human
XX Horost
XX Cytost
XX Cytost
XX O9-AUC
XX 09-AUC
XX 17-JAI
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Best Local :
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SEN The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are use for antenatal diagnosis of human genetic disorders.
    17-JAN-2001; 2001WO-US01354
                                                                                                             cytostatic; gene
                                                                                                                                                                                                                                                                                                                               1361
                                                                                                                                                                                                                                                                                                                                                                                    1301
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                                09-AUG-2001
                                                                                                                                                       Human
                                                                                                                                                                              07-NOV-2001
                                                                                                                                                                                                         AAK87559;
                                                                                                                                                                                                                                     AAK87559 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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                                                         WO200157182-A2
                                                                                                                           Human;
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                                                                                                                                                                                                                                                                                                       387
                                                                                                                                                                                                                                                                                                                                                           447
                                                                                                                                                                                                                                                                                                                                                                                                              507
                                                                                   sapiens
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zing gene expres
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                                                                                                                           immune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-023623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID No 8336; 654pp;
                                                                                                                           haematopoietic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression in
                                                                                                             therapy; vaccine;
                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%;
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                                                                                                                                                                                                                                     10119
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; Pred. No. 0.51
0; Mismatches
                                                                                                                                                    antigen
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n human placenta
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                                                                                                                         immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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No. 0.
                                                                                                             metastasis;
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.51;
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17-MAR-2000
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11-AUG-2000
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2000US-0199076
2000US-0199076
2000US-029451
2000US-0214886
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2000US-0211647
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2000US-0229644
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
  Nucleic acids encoding useful for preventing,
                                                                                                               Rosen
                                                                                                                                                       ( HUMA - )
                                                                 2001-483426/52
                                                                                                            CA,
                                                                                                                                                       HUMAN GENOME
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2000US-0251990.
2000US-0254097.
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2000US-0251868.
2000US-0251869.
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2000US-0250391.
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2000US - 024617.
2000US - 0246475.
2000US - 0246476.
2000US - 0246477.
2000US - 0246477.
2000US - 0246477.
2000US - 0246477.
2000US - 0246523.
2000US - 0246524.
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2000US-0241785.
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2000US-0237037.
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human immune/hematopoietic antigen diagnosing and/or treating cancers
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  polypeptides and
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Best Local S
Matches 84
                  31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

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                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                    09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK73076;
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                                                                                                                                                                                                                                         17-JAN-2001;
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2000US-0179065.

2000US-0186628.

2000US-0184664.

2000US-0186350.

2000US-0199874.

2000US-0199123.

2000US-0198123.

2000US-0205515.

2000US-0214886.
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53.2%;
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Pred. No. 1.9;
0; Mismatches
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0 other;

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Length 10119; Indels

74; 22;

0;

Gaps

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (amino acid sequences given in AAM82170 to AAM91921. (I) have cytostat: activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or delarioss.
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17-NO
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                                                                                                                                         Disclosure;
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                        decreased
                                                                                     cytostatic
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30-JUN-2000
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2000US-0215135 2000US-02116807 2000US-02116807 2000US-0211487 2000US-0212956 2000US-02245118 2000US-02245118 2000US-0225513 2000US-0225266 2000US-0225266 2000US-0225266 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225757 2000US-0225759 2000US-0225757 2000US-0235757 2000US-0235757 2000US-0235757 2000US-0235757 2000US-0235757 2000US-0235757 2000US-0235757 2000US-0235703 2000US-0235836 2000US-0237039 2000US-0237039

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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                   6851 GAAAAAAGTAAATCATCCTGAAGTTAAGTCTTTAATGA 6814
                                                                                                                                                 1361 gaacacccctattcatgttgtaaaggacactttaaaga 1398
                                                                                                                                                                                                                   6911 TTTCATAGAGACAGAGTCTCACTATGTTTCCCCAGTCCTAATAAACATTATGTGATAAAAA 6852
                                                                                                                                                                                                                                            1301 gctaatacagttaaaaaaacggtatttccctggttctgatccaacattatcagtgttaca 1360
                                                                                                                                                                                                                                                                                                           1241 ttcgaagtgactggaataacagtttaatgacagcattaatagctcctgcatatgtgaatt 1300
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                                                                                                                                                                                                                                                                                                                                                                                                          2.8%;
milarity 53.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Score 39.6; DB 22; Length 12247; Pred. No. 2.1; 0; Mismatches 74; Indels 0;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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1: /ggn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Gapop 10.0 , Gapext 1.0
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1401
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US-08-781-891-79
US-08-470-179-1142
US-08-480-640A-225
US-08-686-257A-225
US-08-686-757-1
US-08-08-08-757-3
US-08-9247-3738-3
US-09-247-3738-3
US-09-150-741-1
US-08-1804-12-1
US-08-1804-12-1
US-08-918-190-1
US-08-724-394A-21
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US-08-36-920-245A-1
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Sèquence 14, Appl
Sequence 17, Appl
Sequence 225, App
Sequence 225, App
Sequence 225, App
Sequence 225, Appl
Sequence 1, Appli
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Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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Cation US/0823246 ON: NRE, F. EIFLINGER, F. KNER, F. G. ION: RECOMBINANT NCES: 52 ADDRESS: Oley & Lardner Diagonal Road, S dria  29 29 29 20 Entle FORM: Floppy disk M PC compatible TEM: PC-DOS/MS-D tentIn DATA: UMBER: US/08/232 N: 435 ON DATA: UMBER: US/07/935 UMBER: US/07/935 UMBER: P9 1 114 26-AUG-1991 INFORMATION: Stephen A. 104-26-AUG-1991 ON INFORMATION: Stephen A. 1703)836-9300 3)683-4109 9 10 NO: 14: TERISTICS: base pairs c acid single near E: TERISTICS: C acid esingle near E: t-F1s	14964 1361 1360 1400 1400 1498 1498 1498 2653 2653	5888844
US/082324  EER, F. G. G. G. C. G. C. G. C. G. C. G. C. G. C.	111444100044	132142
2324 ENAN INAN Ole MS- 96 # 11 11 11		- SD - SD - SD - SD
NT FOW Suite Suite #1.0, #1.0, 14.335, 313		08-07-08
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Query Match

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US-08-781-891-79/c
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Sequence 79, Appir
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                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                    REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                            STRANDEDNESS:
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Schellenberg, Gerald D.
INVENTION: GENE AND GENE PRODUCTS RELATED
INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08781891
                                                                                                                                                                                                                                                                                                                                                                                                                E: SEED and BERRY LLP 6300 Columbia Center,
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Pred. No. 0.016;
88; Mismatches
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WS-08-470-179-142

; Sequence 142, Application US/08470179

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49881 ACTGAGGGGGAAAACCGAAGAAAGAATCAGAAATAAAAGAAAAAAATTATAGAAGTCTTC 49822
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Myc
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Huang Ph.D, wai Mun
TITLE OF INVENTION: Method and Compositions
TITLE OF INVENTION: Identification of Specie
                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                  797 gagctctaaatgtgctgtattcagtaaagggcaaaatcacagatggagacagattgaaaa 856
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857 ggaaacaatttcatgcatctgtaattgatagtgttactaaaaagaggcagctcaaagaca 916
                               246 GAGATATACAGAAGCAAGATTATCTAAAATATCTAATGAAATGTTAAAAAAACATTGAAAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sweigert Ph.D, Susan I
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Salt Lake City
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                                                                                                            Score 34.2; DI Pred. No. 1.7;
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                                                                                             Mismatches
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; ANTI-SENSE: N
US-08-480-640A-225
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,678 TELECOMMUNICATION INFORMATION:
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                  1024 tctaaaagtgtcatatc 1040
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CURRENT APPLICATION DATA:
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                                                                             964 ggaaatettaetaegtggetaatttgtaatagateaggetttteaagtatggagaaagta 1023
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                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                           ACATACGATAGTATGTGCTTATTTAAAAACACATCAAACTTATCATGAATAGGTATATTA 101
                                                                                                                      AATAACCAAAATCCAAACATTACATATCTGTGGTCTGATTTCTTTATTTTATCTCTAAGT 161
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Junker, David E.
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48.2%;
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Pred. No. 2
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US-08-488-237A-225/c
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; ORGANISM: Swinepox virus
US-08-686-968C-225
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 225
LENGTH: 305
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APPLICANT: Cochran, Mark D.
APPLICANT: JUNKer, David E.
APPLICANT: JUNKer, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION UNMEBR: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
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Best Local Similarity
Matches 95; Conserv
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                TELEFAX: (2
INFORMATION FOR
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                                   TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
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STREET: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
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FILING DATE: 07-JUN
CLASSIFICATION: 424
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Junker, David E.
                  (212) 391-0525
OR SEQ ID NO: :
                                                                                                                                                                                                                PatentIn Release #1.0,
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48.2%;
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TOPOLOGY: STRANDEDNESS:

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DNA (genomic) single

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                                                                                  INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL:
ANTI-SENSE: N
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STREET: New York
CITY: New York
TI S.A.
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                   NAME: Robinson, Joseph R. REGISTRATION NUMBER: 33,448 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
TOPOLOGY:
                    STRANDEDNESS:
                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.25
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Matches

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US-08-462-949-1
                                                                              US-08-023-764B-1
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              Query Match
Best Local S
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Best Local Similarity
                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
American Cyanamid Company
ADDRESSEE: American Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                         MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL:
                                                                                              ANTI-SENSE:
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 TTGCTATGAAAAAGTCAACAATCTGGATATTAGGCATTATTATGGGTCTTTCCTTTCTGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                          TOPOLOGY:
                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 26-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                        LENGTH:
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              Similarity
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                                                                                                                                                                       nucleic acid
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: United States
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                                                                                                                                                         single
              2.4%;
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Bacteroides Fragilis
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Score 33.8; D
Pred. No. 4.6;
0; Mismatches
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Pred. No. 4.6;
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                           DB 1;
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                           Length 2651;
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                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4203 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/866,757
FILING DATE: 30-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: LI, XIAOTONG
APPLICANT: BERGSMA, DERK J
TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                      524 tgtttagagatttggatgcagattttaggacacagttctcagatgttctggatctttatc 583
                       644
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CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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 aaatggcaaaagtttcggaaatttcgtctgtt 675
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                                                       GAAAATCACATTTTAAAAATAGATTTTTAAAAAATATTAAACAGCTGTTCTTTATCTTGTGC 2748
                                                                                                                                 TGTCCTGAGATTAAGGATGAAACATTAGGTAAAATTAGCAAGATATTTCTTCAGTTATA 2808
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                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                         2.4%;
                                                                                                                                                                                                      Score 33.6; DB Pred. No. 6.3; 0; Mismatches
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                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                           Length 4203;
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; ORGANISM: HOMO
US-09-153-593-1
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US-09-153-593-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ELSHOURBAGY, NABIL A
APPLICANT: LI, XIAOTONG
APPLICANT: BERGSMA, DERK J
TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
FILE REFERENCE: GH-70055-1
CURRENT APPLICATION NUMBER: US/09/153,593A
CURRENT FILING DATE: 1998-09-15
COURENT FILING DATE: 1998-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 08/866,757 EARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4203
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL
                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,747
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
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ADDRESSEE: E.I. DU PONT DE
STREET: 1007 MARKET STREET
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Local Similarity 51.3%;
es 78; Conservation
                                                                                            FILING DATE:
                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                 DELAWARE
                                                                                                                                                                                                                                                            UNITED STATES
                                                                                                                                                                                                        DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                           SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
                                                                                                                                                                                                                                                                OF AMERICA
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TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:

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TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112

SEQUENCE CHARACTERISTICS:

LENGTH:

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                                                                             RESULT 13
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               Sequence 3, Application US/09296715 Patent No. 6171839 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Query Match
Best Local 9
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APPLICANT: O'KEEFE, DANIEL
TITLE O'KEEFE, DANIEL
TITLE O'KEEFE, DANIEL
TITLE O'KEEFE, DANIEL
TITLE O'KEEFE, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/247,373B CURRENT FILING DATE: 1999-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                            LENGTH: 1007
TYPE: DNA
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CLONE: SSM.PK0026.G11
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TISSUE TYPE: SOYBEAN
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APRLICANT:
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                                                                                                                     440 aattagaagaggctttaaagcactggaaaagctattgaaa 479
                                                                                                                                    380 actgaactacattggggagaaagttggccctgatgaaaaacttccttgggcccaaagtat 439
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58; Conserv
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58; Conservative
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DEDNESS: single
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 MCGONIGLE, BRIAN
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Pred. No. 6;
0; Mismatches
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Pred. No. 6;
0; Mismatches
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RESULT 14
US-09-120-365-90
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 1750
                                                                                                                                                                               Sequence 90, Appl
Patent No. 610351
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                      EARLIER APPLIATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SPO TO MOON. 10.
                                                                                                 CURRENT APPLICATION NUMBER: UPGOURRENT FILING DATE: 1998-07-
                                                                                                                                APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
                                                    NUMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 302-773-0164 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
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LENGTH: 1007 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
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CLONE: SSM.PK0026.G11
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Pred. No. 6;
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TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 33290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
EARLIER APPLICATION NUMBER: JP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 90
SEQ ID NO 90
LENGTH: 1750
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Search completed: May 22, Job time: 7551 sec
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US-09-515-039-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Natori, Shunji
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Best Local Similarity 49.1%;
Matches 86; Conservative
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Best Local Similarity 49.1%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Periplaneta americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Periplaneta americana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                              576 atctgcaaatgatcctggtgttaaaaatcgccatcccagttcgatacgaaatgaa 630
                                                                                                                        873 atctgtaattgatagtgttactaaaaagaggcagctcaaagacataccagttcaa 927
                                                                                                                                                                              516 gtttggtggacacaaaaggagccaaggtcaacaaatacacaatgtggattcggtacaaga 575
                                                                                                                                                                                                          813 gtattcagtaaagggcaaaatcacagatggagacagattgaaaaggaaacaatttcatgc 872
                                                                                                                                                                                                                                                                456 taacaggattcaagttgattggtacagaaccaataaatggcctgaattgcgaaaaatggc 515
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Pred. No. 8.5;
0; Mismatches 89;
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Pred. No. 8.5;
0; Mismatches 89;
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Perfect score:
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Maximum DB seq length: 2000000000
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Match Length DB
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1: gb_ba:*
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## ALIGNMENTS

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                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12793)

Hudson, T.J., Engert, J. and Richter, A.
Identification of arsacs mutations and methods of use therefor Patent: WO 0129266-A 1 26-APR-2001;
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)

Location/Qualifiers

1. 12793
                                                                                                                                                                                                                                                                                            AX119931 12793 bp
Sequence 1 from Patent WO0129266.
AX119931
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                4163 a
            /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 12793)

Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Ge, B., Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A.

ARSACS, a spastic ataxia common in northeastern Quebec, is caused by mutations in a new gene encoding an 11.5-kb ORF

Nat. Genet. 24 (2), 120-125 (2000)
                                                           Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital, 1650 Cedar Ave., Montreal, QC H3G 1A4, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            AF193556 12793 bp
Homo sapiens sacsin (SACS) gene,
AF193556
                                                                                                  Direct Submission
                                                                                                            Richter, A.
                                                                                                                       Engert,J.C.,
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            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="between D13S232 and D13S292"
                                                                                                                        Berube,P.,
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                                                                                                                       Dore,C.,
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                                                                                                                        Ge,B.,
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                                                                                                                        Hudson, T.J.
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SANQLVVPEGDYLLPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSAFVP
LLSCHTANIESTSILKALHYMYGTSTFAEKLVENGYTKYRCHUNHLMSQDDI
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VINLEYESDFKPYLYKLPLEGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ
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KVSEISSVPASDRMVQNLLDK/KRSDGABLLMFLKHMEKISICEIDK/STALNVLYSVK
GKITDGDRLKRRQFHASVIDSVTKKRQLKDIPVQOITYTMDTEDSEGNLTTWLLCURS
GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH
VNGHFALDSARRNLWRDDNGVCPRSDMNNSLMTALIAPAYVELLIQLKKRYFPGSDPT
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PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY
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SVDDGITLYGENITNACYKYLHEALMQNEITKHSIIDKLKFFSFILVENAYVDSSKYS
EHLUNEBAAPLLYGLPHKYKNNERELEFSTVGVROSCTVEDFALVLESILOPERGTKQITE
ENFQLCRIISEGIWSLIREKKOEFCEKNYGKILLPDTNLMLLPAKSLCYNDCPWIKV
KOTTVKYCHADIPREVAVKLGAVPKRIKALERYASINVCFTLGTEFGQKEKLTSRIKS
ILNAVESEKEMKLKELLONADDAKATEICFYDDPROHPVDLIFDDKWAPLOGPALCYN
NOPFTEDDVRGIQNLGKGTKEGNPYKTGQYGIGFNSYYHITDCPSFISGNDILCIFDP
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KEIWKTDTKGRNUTTFNRHVIVKAYLQVLSVLKDLAFTGSELMDYTYYAWPDPDLVHD
DFSVLOQGFYEDDIAHGKRELITKYPSDGSTWYSKNWRFLDDSILKRRDVGSAAFKIF
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ILLSLIDEKLKIRDPRAKDFAAKYQTIRFLPFLTKPAGFSLDWKGNSFKPETMFAATD
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TECSFLIDMRRNDIRENLIDPEMAACHGPALMSFNNSQFSDSPVNITRLGESIKRG
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ALNTPVLSVLKEAAKLMATCGSSSNKLPSDEPSKSCILJTVEEFHHVERIADLQSV
LFRGPDDDPAALFEMAKSGQSKKPSDELSQKTVECTTWLLCTCMDTGEALKFSLSESG
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GKLPCRLQQTNLKLFHSIKLLVSKORTOKENEIEVEGLPLLITLDSVLQTFDAKRK
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PNTPVPIHHSKNPSKLIMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE
EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL
                                                                                                  LDPNEMRTYKRVYSGLFRSLQNDSYKVRSDLENVRDLALYLPSQDGRLVKSSILVFDD
APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE
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HSLRQIGLKNEASLKEKDYYQYAKKIEALQYGACPDQDYLLKKAKTLLLYLNKNHTLL
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TDSSEKEKRIIQELAIFKRINHSSDQGISSYTKLKGCKVLHHTAKLPADLRLSISVID
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TLfDEMpLIPRTILEEGQTCVELIRLRIPSLVILDDESEAQLPEFLADIVQKLGGFVL
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/protein_id="AAF31262.1"
/db_xref="GI:6907042"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500;
                          requests: clonerequest@sanger.ac.uk
On Apr 12, 2001 this sequence version replaced gi:12709868.
During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                     Human DNA sequence from 13q12.11-12.2, complete AL157766
                                                                           Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                         HTG
                                                                                                                                                                                                                                                                                                     AL157766
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that
                                                                                                              Direct
                                                                                                                                                            Mammalia;
                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                          AL157766.9
                                                                                                                           Fromans, A
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Pred. No. 6.9e-101;
                                                                                                                                                                                                                                                                    92693 bp DNA ....
n clone RP11-40020 on chromosome
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                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers give in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-760Ml is at 92594 in this sequence.
The true right end of clone RP11-72P19 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
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This sequence was finished as follows unless otherwise noted: all
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/note="AluSg1 repeat:
24769. .24891
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/note="MIR repeat: matches 37963. .38254
                                         /note="AluSx repeat: matches 1. 37202. .37414
                                                                                                                                                                                                                                                                   26938
                                                                                                                                                                                                                                                                                                          /note="L2 repeat: 26245. .26344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 1. .310 of consensus" 19644. 19873
/note="MER46A repeat: matches 1. .235 of consensus 20613 .20912
                                                                                                                                                                                                                                                                                                                                                        26033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER46C repeat: matches 1. .286 of consensus" 18986. .19294
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                                                                                                                                                                            28522.
                                                                                                                                                                                                                     /note="MIR repeat: matches 3.
27150. .27653
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                                                                                                                                                                                                                                                                                                                                                                                                  25871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSg1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 81.
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                                                                                                                                                       /note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat:
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                                                                                                                                                                                                                                                                                      matches 2154.
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                                                                                                                                                                                                                                                                                                                                                                           matches 2356.
                                                                                                                                                                                                                                                                                                                                                                                                                      matches 2554.
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                      22.
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/notce="TIGGER1 repeat: matches 2238. .2418 of consensus"
62188. .62316
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61036. .61144
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note-"Single clone region. Assembly confirmed by restriction digest data."
                                                                                                                                                                                /note="Aluy repeat: matches 1. .129 of consensus"
62330. .62363
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47477. .47873
/note="AluY repeat: matches 1. .306 of consensus"
                    /note="TIGGER1 repeat: matches 46. .1586 of consensus"
54386. .64694
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=="30 copies 2 mer ga 75% conserved"
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10444. .40733
                                                                           note="AluSq_repeat: matches 1.
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                                                                                                                                         'note="Alu repeat: matches 261. .294 of consensus"
32362. .62565
                                                                                                                                                                                                                                                                                                                                                         'note="AluSq repeat: matches 129. .313 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                  note="24 copies 2 mer ca 93% conserved"
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16754. .47052
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4790. .45101
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5261. .45312
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78. .54137
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e="CpG island"
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0. .49693
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8. .49212
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agacatgtgtggaactcattagactcaggattccatcgtt 300 	aactatactagaggaaggtc 	241 18669	g 84
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atcacccatctgtttcatggcttaagatggtttggaaaaa 180 	tccatttgatgaaaacagaa 	121 18789	95 79
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internal repeat: matches 332739	consenset_region 72454.	repe	
Alusx repeat: matches 1295 of consensus" .72256 MER31-internal repeat: matches 42175 of	/note= at_region 72145. /note=	epe	
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1413 R21B repeat: matches 548680 of consensus" 1737	at_region 71279. /note= at region 71411.	repe	
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pies 4 mer tgtg 82% conserved"	/note= at_region 67586.	epe	
PB2 repeat: matches 57896155 of consensus" 6410	at_region 66371.	repe	
es 2 mer ta 100% conserved"	at_region 65696.	epe	
repeat: matches 57285791 of consen	at_region 65571. /note=	repe	
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ER1 repeat: matches 2946 of consensus"	/note="1 at_region 65068	epe	
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Waterston, R.H.
Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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1 (bases 1 to 99819)
Waterston,R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fernandez,C., Ferraguto,D., Forcum Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,F., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hoggen,A.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hoggen,A.,
Milliamson,A., Weng,G., Golden, M., Milliamson,A., Weng,G., M., Milliamson,A., Weng,G., Man, M., Milliamson,A., Weng,G., Milliamson,A., Weng,G., M., Milliamson,A., Weng,G., Milliamson,A., Weng,G.,
                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-MAY-2000) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Sep 12, 2001 this sequence version replaced gi:14787161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, C., Delgado, O., Delgado,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 174140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny,D.M., Rives,M., Scherer,S., Sodergren,E.,
Worley,K. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC069017.20 GI:15559167
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 174140)
                                 Center: Baylor College of Medicine Center code: BCM
Center clone name: MGS3-342I16
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clone MGS3-342I16,
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NFT SEQUENCE, 5 unordered
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cine, One
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BASE COUNT
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Best Local
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                                                55616
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    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 tgatttacaggaagaccatgtactcagctgcagcttctaaatccagaacgatttgcacgt 61
                                                                                                                                                                                                                               aaaatatattcattcaccattaccaagtgctgttttgcagataatggagaagatgccatt 480
                                                                                                                                                              gtcattttagacgatgaatctgaagcacagcttccagaatttttagcagacattgtacaa 361
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATCTTCAGGAAGACCATGTACTCAGCTGCAGCTTCTAAATCCAGAATGATTTGCATGT 55319
                                             AMACTTG--GGAGTAGTCCTGAAAAGACTAGATACCTCTATTCAGCATCCACTGGTTAAA 55673
                                                                          aaacttggagggtttgtccttaaaaaattagatgcatctatacaacatccgcttatt-aa 420
                                                                                                                                         GTCATTTTAGATGAAACTGAAGCTCAGCTTCTAGAATTCTTAGCAGATATTGAACAA 55615
                                                                                                                                                                                                                                                                                                                                                                                                                      CCATTTAGTGAAGACAAACATCACCCATCCCTTTCATGGCTTAAGA----TTGGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTATTAAAGAAGTCATGAATAAATTCTGGCGTGGTGGAGAGTTGTTGGTTCAGTGCTAT 55379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; L08821

Chemistry: Dye-primer Bodipy: 37% of reads

Chemistry: Dye-terminator Big Dye: 63% of reads

Chemistry: Dye-terminator Big Dye: 63% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 17525 bases at least Q40

Consensus quality: 179254 bases at least Q20

Consensus quality: 181014 bases at least Q20

Estimated insert size: 178322; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 7.4x in Q20 bases; sum-of-contigs estimation
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/clone="MGS3-342I16"
32907 c 34252 g 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168914: gap of unknown
174140: contig of 5226
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Pred. No. 1.3e-66;
"":cmatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by mutations in a new gene encoding an 11.5-kb ORF Nat. Genet. 24 (2), 120-125 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 11493)
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                                                                                                                                                                                                                                   LVESVHVNLEQALSIFTKPTINAVLKHFKTVVDWYTSKTFSDEDYYQFOHILLETYGF
MHDHLSEGKDSFKALKFPWVATGKNFCPLAQAVIKPTHDLDLOPYLYNVPKTWAKFHQ
LFKACGSIEELTSDHISMVIQKVYLKSODELSEEESKONLHLMLNIMRWLYSNOIPAS
PNTPVPTYHSRNPSKLYMKFHHECCYCDIKVDDLNDLLEDSVEPTIILVHEDIFWKTAE
MLKVPCLSTRLINPENMGFEQSGQREPLTVRIKNILEEYPSVSDIFKELLONADDANA
TECSFMLDMRRNMDIRENLLDEGMAACHGPALMSFNUNSEFSUSPFLNITRLGESIKRG
EVDKVGKFGLGFNSYVHITDIFIIMSREFMINEDPNINHISHIIKDRSMPGIKINWSK
KOKKLRKFPNOFKFIDVFGCOLPLAVBAPYSNGTLFRLSFRTQQEAKVSEVSSTCY
NTADIYSLVDEFSLCCHRLIIFTQSVNSMYLKYLKIEETNPSLADDTIINKKYCPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSNYLDWLMPLKFIHMSQGHVVAAGDLFDPDIEVLRDLFYNEEEACFPPTIFTSPDIL
HSLRQIGLKNESSLKEKDVVQVARKIEALQVSSCQNQDVLMKKAKTLLLVLNKNQTLL
QSSEGKMALKKIKWVPACKERPPNYPGSLVWKGDLCNLCAPPDMCDAAHAVLVGSSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNTFWPGRELVVQWYPFSEDKRHPSLSWLKMVWKNLYIHFSEDL
TLPDEWPLIPRTLLNEDQTCVELITLRIPSVVILDDETEAQLPEPLADIYQKLGGIVL
KRLDTSIQHPLVKKYIHSPLPSAILQIMEKIPLQKLCNQIASILPTHKDALRKFUSSL
TDTSEKEKRIIQELTIFKRINHSSDQGISSYTKLKGCKVLDHTAKLPTDLRLSVSVID
SSDEATIRLANMLKIEKLKTTSCLKFVLKDIGNAFYTQEEVTQLMLWILENLSSLKNE
GRFPYGSTQDYLNPIILIKLVQLGMAKDDILWDDMLERAESVAEINKSDHAAACLRSS
ILLSLIDEKLKIKDPRAKDFAAKYQTIPFLPFLTKPAGFSLEWKGNSFKPETMFAATD
                                                    LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKQILLENTFSEKQFFSEVFFPNIQEIEA
ELRDPLMNFVLNEKLDEFSGILRVTPCVPCSLEGHPLVLPSRLIHPEGRVAKLFDTKD
                                                                                                      RRLGLVPCGAVGVLLHETQEQKWTVKPHIGEVFCYLPLRIKTGLPIHINGCFAVTSNR
KEIWKTDTKGRWNTTFMRHVIVKAYLQALSVLRDLAIGGELTDYTYYAVWPDPDLVHD
DFSVICKGFYEDIAHGKGKELTRVFSDGSMWYSMKNVRFLDDSILQRKDVGSAAFKIF
                                                                                                                                                                                    ALNAPVLSVLKEAAKLMKTCSSSNKKLPTDVPKSSCILQITVEEEFHHVFRRIADLQSP
LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTVDCTTWLICTCMDTGEALKFSLNESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="sacsin"
/protein_id="AAF31263.1"
/db_xref="GI:6907044"
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Sciurognathi; Muridae;
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Query Match Best Local S Matches 366 ccattaccaagtgctgttttgcagataatggagaagatgccattgcagaaattgtgtaat AAACGTCACCCATCCCTTTCATGGCTTAAGATGGTTTGGAAGAATCTCTATATACATTTC atgaatacattctggcctggcagagaattgattgttcaatggtatccatttgatgaaaac 136 GAAACTGAAGCTCAGCTTCCAGAATTCTTAGCAGATATTGTACAAAAACTTGGAGGGATT gaatctgaagcacagcttccagaatttttagcagacattgtacaaaaaacttggaagggttt GACCAGACGTGTGTGGAACTCATCAGACTCAGGATCCCATCAGTAGTCATTTTAGATGAT ggtcagacatgtgtggaactcattagactcaggattccatcgttagtcattttagacgat Similarity Conservative LESLLIIHDANNRLKQAKHFYDRTVRVFEVMLPEKLFIPKEFFKKLEQVIKPKNQAAF
MTSWYEFLRNIGLKYALSQQOLLQFAKEISVRANTENNSESTLQSTVDILLHHIFQER
MDLLSGNETKELSLIPFLCPERAPAEY IRFHQYGEVNGTLPLIKFNGAQVNPKFKQC
DVLQLLWTSCPILPEKATPLS IKEQEGSDLAPQEQLEQVLNMLNVNLDPPLDKYINKC
RNICNITTLDEEMVKTRAKVLRSIYEFLSAERBEFRFOLRGVAFVMVEDGWKLLKEEE
VVINLEYEADFKPYLYKLPLELGTFRQLFEGEDIISTKQYVEVLSRIFKSSEGKQ
LDPHEMRTVKRVSGLFKSLQNDSVKYRSDLENARDLALXLPSQDGKLVKSSILVFDD
APHYKSRIQGNGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE
ETPKVCQFGALCSLGKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDKSDINFLL
ALAMTLKSATDNLISDTSYLIAMLGCNNIYRISEKLDSLGVKYDSSEPSKLELPMFGT
PABEIHYTLLMDPMNVFYPGFFVGYLVDAEGGDIYGSYQDTTTTATIVQEVEREEDAD
PHPAEIHYTLLMDPMNVFYPGFFVGYLVDAEGGDIYGSYQDTTTTATIVQEVEREEDAD FHLNFEAAPYLYQLPNKYKNNFRELFESVGVRQSFTVEDFALVLESIDQERGKKQITE
ENFQLCARIISEGIWSLLREKRQEFCEKNYGKILLPDYNLLLLPAKSLCYNDCPWIKV
KDSTVKYCHADIPREVAVKLGAIPKEKKALERYASNICFTALGFEFGQKEKLTSRKY
KDSTVKYCHADLPREVAVKLGAIPKEKKALERYASNICFTALGFEFGQKEKLTSRKY
ILNAYDSEKEMLKELLQNADDAKATEICFVFDDRQHPVDRIFDDKWAPLQGPALCVYN
NQPFTEDDVRGIQNLGKGTKEGNPCKTGHYGIGFNSVYHITDCPSFISGNDILGIFDP
HARYAFGATSVSPGRMERDLDADFRTQFSDVLDLYLGNHFKLDNCTMFREPLRNAEMA AQKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMEC TACIIIKLENFIQOKV" LYLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRPQS DKYSFQRFYTSWNQEATSHKSERQQQSKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEA RRWLRQARANESAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTAL STSQLVVPEGDVLIPLSLMHIAVFPNAQSDÄVFHALMKAGCIQLALNKICSKDSALVP LLSCHTANIDSPASILKAVHYMVQTSTFRTEKLMENDFEALLMT YNCNLSHLMSQDDI KILKSLPCYKSISGKYMSIAKPGTCYVLTKSTPESAEVEMVTQSSSSAFLEEKVHHKEK YEVLGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLASIEEPSEIKEQLFEK GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEESEFEVEGLPLLITLDSVLQIFDGKRPK FLTTYHELIPSRKDLFMNTLYLKYSSVLLNCKVAKVFDISSFADLLSSVLPREYKTKN CAKWKDNFASESWLKNAWHFISESVSVTDDQEEPKPAFDVIVDILKDWALLPGTKFTV VNGHFALDSARRNLMADDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYSCHEDMKRLLPVVRA PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLDDELQHLKNADYNITERKTVAENVY RLKHLLLEIGFNLYYNCDETANLYHCLVDADIPVSYVTPADVRSFLMTFSSPDTNCHI QVSEISSVPSSDRMVQNLLDKLRSDGAELLMFLNHMEKISICEIDKATGGLNVLYSVK GKITDGDRLKRKQFHASVIDSVTKKRQLKDIPVQQITYTMDTEDSEGNLTTWLICNRS GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH NTSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPDESSQNRDSAPTTPTSPTEFLTPGLR SIPPLFSGKESHKSPSTKHHSPRKLKVNALPEILKEVTSVVEQAWKLPESERKKIIRR 66.2%; a 0; Score 331.2; DB 10; Pred. No. 1.4e-63; 0; Mismatches 58; g Length 11493; 0; 436 60 180 120 376 316 496 300 240 256 0;

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         AE001381 12029 bp
Plasmodium falciparum chromosome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 11492)
Hudson,T.J., Engert,J. and Richter,A.
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Sequence 3 from Patent W00129266.
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AX119933.1 GI:14036679
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1 (bases 1 to 12029)
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4;282(5395):1827]]
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KKSPSILFIVFSVMSILTFFFFFFKETKGGEIGTSPYITMEERQKHMTKSVV"
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complement(3799...5049)
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                                                                                                                                                                                                                                                                                                                                                                                                    YIFDIYKCDNVYLFINYIKDILECDDIIKVTHDCREDCSILYNQYNIHLKNILDTQVA
YNLLLKNNNNYTNTYQISYDDLLKKYLFINNNHKIYFHKMITLDNYIYLKRPIMKELI
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KNKEHNVITQKDNAKMDNIDEQ"
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KVEEKQKYNDEDGKENVSIDNVEECNKMKDEYDKKENNVSNIEEENI ILDSKEQNI IL
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/gene="PFB0230c"
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CNNDKVKLEEYHHEKELNNVQIINDMDIKKNEAKKEKNNKKKEKQKNKKNEKEKNKKK
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FKRYKEKYKKKKKKLHISSKRKKDKRNLDLYCKKKKKEIIYTHLFLPTRLREKINKS
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KYSPPHSRRNRIYFYPYTKLLRRKRLRRISHFKEDRYVIHKGPLTKKKKKKIYINKKY
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ITYTTMTMGIVSIHSAYKLV"
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FRILEKSKFYLKKNNQSIPFDHISYQQYLPHIIVCDVNNDMLNVGKKKAATLGYDQNL
TWLVQNAENLESVESNSIDVITLSFGIRNFTNIPQALKEIHRVLKPGGRFLCLEFSKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rattus norvegicus clone CH230-38P14, *** SEQUENCING IN PROGRESS
***, 61 unordered pieces.
AC096291
                                findPhrapList
Consensus quality:
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On Dec 20, 2001 this sequence version replaced gi:15627911
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Direct Submission
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                                                                                                                                                                                                           Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
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                                                                                            Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                           Center clone name: CH230-38P14
   Consensus quality:
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83123 bases at least Q40
91227 bases at least Q30
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Consensus quality: 96818 bases at least Q20 Estimated insert size: 71455; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 0.9x in Q20 bases; sum-of-contigs est:
        Q20 bases; sum-of-contigs estimation
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\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved. arbitrary. Gaps between the contigs are represented as 19885 12963 22063 22163 225153 227940 30904 31004 31004 31493 33493 33493 336533 336533 336533 336533 347353 47353 47353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 5735 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57355 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57353 57355 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5735 5 63823 65056 65156 66344 66444 67897 67997 62242 63723 60422 62142 55834 57173 57273 58477 58577 60322 11674 11774 14735 14835 18013 18113 3917 38963: gap of (42247: contig 42347: gap of (43940: contig 43940: gap of (47352: gap of (47352: gap of (52302: contig 52302: contig 52427: gap of (54327: gap 18012: contig 18112: gap of 19884: gap of 19984: gap of 22062: contig 22162: gap of 25152: gap of 25152: gap of 27939: contig 28039: gap of contig 31003: gap of 33492: contig 33592: gap of 33592: gap of 3632: gap of 3683: contig 58576: 55833: 11773: gap of 14734: contig 11673: contig of 4379 bp in length .4834: gap of 3916: contig 4016: gap of contig gap of gap of gap of gap of gap of contig gap of unknown of 1925 unknown of 3284 of 1720 of 1339 of 1493 of 2231 of 2787 of 2890 of 1772 of 3916 of 1233 unknown of 1481 unknown of 1745 of 1204 unknown of 1306 of 2098 of 2752 of 3312 of 2940 unknown of 2489 of 2864 unknown of 2078 unknown of 3178 bp of 2961 unknown unknown of 3178 unknown bp in l bp in l bp in . length bp in l bp in length pp in ďα bp in dq ģ đđ dq đď đđ bp in dα ďď bp in dq bp in bp in bp in bp in bp in bp in length length

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Query Match
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 caccattaccaagtgctgttttgcagataa
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                                          TGAATAATAATTAAATTCAACTCTACTATTTATTCAAAATAAAAAGTTTAGCAAGA
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KEYWORDS
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CEY39A1A/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75175 TACAGAAGAAATTTCTGACTTGCACATAA 75146
                                                                                                                                                                        gene
                                                                                                                                   CDS
                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone Y39A1A. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-SEP-1998) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans cosmid AL031633 z99293 AL031633.1 GI:3646884
                                                                                                                                                                                                                                                                                                                                                                                                   neighbouring submissions.

The true left end of clone Y39Al is at 1 in this sequence. The true left end of clone W09DlO is at 110854 in this sequence. The start of this sequence (1...106) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadora
Rhabditoidea; Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                 the specified clone. It may be shorter because overlapping sections once, or longer because we overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biolog
Science 282 (5396),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG.
                                                                                                                                                                                                                                                                                                                                   For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                               of sequence Z93785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predictions
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                                                                                                                                                                                                                                                                                                          IMPORTANT:
                                                                                                                                                                                                                                                                                                                       name=Y39A1A
                                                                                                                                                                                                                                                                                                                                                                           The end of this sequence (110854. .110960)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wall,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The C.elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e C.elegans Sequencing Consortium (bases 1 to 110960)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (sites)
                                                                                                    complement(join(1078. .1247,2168. 3561. .377,4206. .4296))
//gene="Y39A1A.1"
.561. .377,4206. .1247,2168. .3561. .377,4206. .4296))
//gene="Y39A1A.1"
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                                                                                                                                                                                      /clone="Y39A1A"
                                      /protein_id="CAA21019.2"
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                                                                                            /note="cDNA EST EMBL:T00867
                                                                                                                                                                                                   /chromosome=":
                                                                                /codon_start=
                                                                                                                                                                                                                /db_xref="taxon:6239"
                                                                                                                                                                                                                           organism="Caenorhabditis"
                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                          This sequence is NOT necessarily the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Genefinder (P. Green, U. Washington),
                                                                                                                                                                                                                                            .110960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematoda; Chromadorea; Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                           overlaps with the start
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/gene="739A1A.5b"
/gene="739A1A.5b"
/note="CDNA EST yk112f11.3 comes from this gene
cDNA EST yk112f11.5 comes from this gene
cDNA EST yk68h1.5 comes from this gene
cDNA EST yk68h1.5 comes from this gene
cDNA EST yk451e4.3 comes from this gene
cDNA EST yk437d12.3 comes from this gene
cDNA EST yk437d12.5 comes from this gene
cDNA EST yk437d12.5 comes from this gene
cDNA EST yk437d12.5 comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQVALNCQGTLVATGSTKGTVIRVFDARTKGPLYELRRGTVQAHLQCMAFSPCSSYLA
VASDKGTLHMFGIRDAEPQKKKNVLERSRGSSSIVKIQLDRPVMAIGFGKKTFKNLQS
IIAICADATYWRHEFYKDNTGNFTSHFGSYDELIEVANDSSFFRTPVE"
                                                                                                                                                                                                                                                                                                                                                                                                          SDDDLEKMLAVIKETVDFYPTDEYMNMKQSIFAEEKETADILVSLSRQSSESGRGTLT
DTQPSTPQPDTSLESPLIAEIQAINLTSSGNQEHGGEGLGAAGPILEEMEALVLKIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(14209. .14677,14977. .15126,15303. .15440,15752. .16004, 16352. .16433,16754. .16939,18701. .19006)
/gene="Y39A1A.5a"
/gene="Y39A1A.5a"
/note="contains similarity to Pfam domain: PF02204
(Vacuolar sorting protein 9 (VPS9) domain), Score=36.7, E-value=1.7e-07, N-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"Sptrembl:09xx24"
/translation-"MEIPIFQEIFIVFVLTIPPDCFQTPHKVMSDKHGEEDKKAKMHL
/translation-"MEIPIFQEIFIVFVLTIPPDCFQTPHKVMSDKHGEEDKKAKMHL
KANDLLCVNGCGFYGTPQWENRCSKCWRAHQNEMKKCQDFAKNRSLLSFDQFQERRKS
TTESKSRGIKNLFKTSPIPEGGTSSPTSTSPASTPTRFEAVVCKTKTNFSAISSIFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(7136. .7306,7430. .7540,7620. .7670))
/gene="x39A1A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(7136. .7306,7430. .7540,7620. .7670))
                                                                                                                                                                                                                                                                                         Join(18036. .18110,18701. .19006)
/gene="Y39A1A.5b"
                                                                                                                                                                                                                                                                                                                                                        HHAKHRSKMDSALKAASQN"
                                                                                                                                                                                                                                                                                                                                                                                 IFKKQAAGNTVSASKRGSTQSPVIRTAEASTQRASPAIAQVEKFESVRQPREPRSRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKSEFEAYTSGHLAPPLSVINSACNQAIYVLEGTIETITNVAKKAGSLAKNLTNMHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Y39A1A.5a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(14209.
16352. .164
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join(8497. .8559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10365.
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PKYPQNDAILCGQQPPPPPHKSTIKTVFKKELMEIPIPVDIEMFRAIQKLVKDGRGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA21018.1"
/db_xref="GI:3880845"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMIFDVARNEEYFEITTPSRYGPITNIHVSPNRLVALNPNRMFVWTYPDDIKQIRSED
IRSNPKGISAMSYDPTTAACYLAYPGFKTGSVQIMHLNALTARESKSPIVIEAHLTDI
                                                                                                                                                                                                                                                                        join(18036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA21016.1"
/db_xref="GI:3880843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Y39AlA.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )oin(8497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST yk210c11.5 comes from this gene EST yk532c5.5 comes from this gene EST yk556b4.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST yk210c11.3 comes from this gene EST yk210c11.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .10416,10699. .10768)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )9. .14677,14977. .15126,15303. .15440,15752. .16004,
_6433,16754. .16939,18701. .19006)
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                                                                                                                                                                                                                                                                        .18110,18701. .19006)
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                                                                                                                                                                                                                       gene
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     δõ
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                             Query Match
                                                         17534 CCAGGTTTTTTTCCAACATTTTTCAAAATGAGATTTAAAATTTTTTTGATAATTTTTTTCC 17475
                                                                                                                                                                                                                       165
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CDS

gene

CDS

225

Local Similarity

8.3%; 48.7%;

Conservative

0,

Score 41.6; DB 3; pred. No. 9.4; 0; Mismatches 119;

Length 110960; Indels

0;

Gaps

0;

agatggtttggaaaaatctttatatacattttttcagaggatttgactttatttgatgaga 224

AGAAAAATTAAAAAACTTCCAAACTAAAAATTTTGAAAAAATCTGGAAATTTTTTGCATTTT 17535 tgccacttatccccagaactatactagaggaaggtcagacatgtgtggaactcattagac 284

285

tcaggattccatcgttagtcattttagacgatgaatctgaagcacagcttccagaatttt 344

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CDS
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                          RNITYVFASTILLPIFYQMKGDIEVTMKVTDDGLTIRNFHSLDGVTMFNMGVEKGAKKV
KTETTITCEKLTRHKIQIPVEFSFSIKEFLSIVTFADQLGSEVCMYYDLPGKPLIVSI
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/db_xref="GI:14530622"
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DPKAERMAVKLQMNYGKKISCRIFEKLAEFSDIERTIHAKLREMGSMLHKPTYNRSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:Q9XX25"
/translation="MTSITSAFLLLLEVAVACRSVPCLDGCTCELSEHDPVIRCDGV
/translation="MTSITSAFLLLLLEVAVACRSVPCLDGCTCELSEHDPVIRCDGV
GLNRRPLPHSSPLRGEHELALTCNDIDTIPAISMIKASFPDLQGIDVQGNTRLMCSDL
VHLHKDIPVLSDCDNEKPLQCDNLDKNCDWKCRTLTKLKEMWAQFKDLVNRKAKEWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(22174. .22353,23082.
/gene="Y39AlA.7"
/note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLRVPKLQKDEOLSSKVYFAÞEMDLEKKPNLDEGFVAPLKGVGMTPEKÆEYYNKVVMP
PNYIVÞETGLFAFKEVEHCKESVHFSPKRMMAACQLVMKMUDEAITQLDMQOLKACN
LLMDIIKKAKRAÐDEFHIEVESQMYVADAFÞVGSNIVKGARRHAHDMWNIIKYRYRI
IFVRLEEGPAÞQQKQRHPQKNGMDHMDEYYNYLRSRTVKYSI
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CDNA EST yk556b4.3 comes
CDNA EST yk540g3.5 comes
CDNA EST yk541e1.5 comes
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27339...27744,28541...28596,28650...28832,28993...29064,
29500...29707,30169...30268,30345...30355)
/gene="x39AlA.23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(25750. .25789,25839. .25909,25963. .26088,26137. .26405,
27339. .27744,28541. .28596,28650. .28832,28993. .29064,
29500. .29707,30169. .30268,30345. .30355)
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join(1950°
SSSGTQKSKKCSESLSQEETTRSQSLPSRNRFVPEIPVAEQSWRDREVTVYEQREPSP
                                                                                                                                                                                                                                                                            cDNA EST EMBL: AU112975 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Y39A1A.23"
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/db_xref="GI:3880842"
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/db_xref="GI:3880849"
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LKIASIFKKQAAGNTVSASKRGSTQSPVIRTAEASTQRASPAIAQVEKFESVRQPREP
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/db_xref="GI:3880847"
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/translation="MLRVLVRTGSEACRAVSTSTAVLSVHPVVKSEDLSAKEIWDRRS
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Direct Submission

Submitted (09-JAN-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,

On Aug 9, 2001 this sequence version replaced gi:14670156.

On Aug 9, 2001 this sequence Transcript Genome Sequencing Center
                                                                                                                                                               all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomlinson,C., Abbott,A., Hawkins,M., Dixon,R. and Boyer,E. The sequence of Homo sapiens BAC clone RP11-785F11 Unpublished (2001)
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (20-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Sulston, J. E. and Waterston, R.
                                                                                                   MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                       between neighboring data submissions.
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                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0785F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP11-785F11.
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7558. .89
/rpt_family="L1"
16440. .16743
                                  /rpt_family="(A)n"
16128. .16439
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15199
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14049
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13396
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13375
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11039. .11289
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10114. .11038
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9388. .9484
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9235. .9420
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8937. .9234
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. .14187
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Вb
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Best Local Similarity
19161 CACTAATTTATAACAAAGATCCCTATGCAATTCAATGTGGAAAAAAATCTGGGAGACAC 19220
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           123 catttgatgaaaacagaaatcacccatctgtttcatggcttaagatggtttggaaaaatc 182
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38783
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23692
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23018
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18356. .18659
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18884
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17413 ...17440
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16916. .17257
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16744. .16874
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4. .21497
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3. .21237
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3. .32523
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                                             Score 41.6; DE Pred. No. 8.8; 0; Mismatches
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                                                                                                                                                                                                                                                                                         "(CA)n"
                                                                    DB 9;
                                              124;
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AC020669/c
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TITLE
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19341 AAACATTGGAGATTATTTTATAAGTAGTTCTTAAACTAGATTCAAAAAAGCACTAAACATA 19400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Gardyna, S., Cant, G., Hagos, B., Heaford, A., McRernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Kothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Diemer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctatactagaggaaggtcagacatgtgtggaactcattagactcaggattccatcgttag 302
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AC020669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6751804. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168982)
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                             Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 167391 bases at least Q30 Consensus quality: 168505 bases at least Q30 Consensus quality: 168505 bases at least Q30 Consensus quality: 168505 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L1948
Center clone name: 114_M_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                        Quality coverage:
                                                                        Insert size: 168000; agarose-fp Insert size: 168582; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Project Information
6.0 in Q20 bases;
6.0 in Q20 bases;
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sum-of-contigs
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KEYWORDS
SOURCE
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ORIGIN
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ORGANISM
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                                                                                                                                                                                                                                                                                                             64018 TAATTCAAGATGGATTTTACACTAATATGTGAAAGATAAGACCACAGAGTCTATAGAAGA 63959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 catttgatgaaaacagaaatcacccatctgtttcatggcttaagatggtttggaaaaatc 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                 AAACATTGGAGATTATTTATAAGTAGTTCTTAAACTAGATTCAAAAAAGCACTAAACATA 63899
                                                                                                                                                                                                                                                                                                                                                 ctatactagaggaaggtcagacatgtgtggaactcattagactcaggattccatcgttag
                                                                                                                                                                                                                                                                                                                                                                                          TGGATATGCATTTAGAAAAAAAAATGAATTTTAGCTCTCCCACATACCATATCCTGAAAT 64019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116;
Homo
                                      HTG;
                                                                                 איט טעט טעט טעט DNA linear HTG 30-JAN-2002 Homo sapiens chromosome 4 clone RP11-814T21, WORKING DRAFT SEQUENCE, 2 unordered pieces.
AC107486
                                                        AC107486.2 GI:18425346
                                                                               AC107486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93503 93602: gap or
93603 168982: contig of 75380
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21387 38403; contig of 17017 bp in
38404 38503; gap of 100 bp
38504 93502; contig of 54999 bp in
93503 93602; gap of 100 bp
sapiens
                                    HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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38504. .93502
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93603. .168982
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/clone="RP11-114M4"
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)9: gap of 100 bp
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183 tttatatacatttttcagaggatttgactttatttgatgagatgccacttatccccagaa 242
                                                                                                                                                        Local Similarity 48.3 les 116; Conservative
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On Jan 30, 2002 this sequence version replaced gi:18254450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 176000; agarose-fp
Insert size: 206135; sum-of-contigs
Quality coverage: 13.68 in 020 bases; agarose-fp
Quality coverage: 11.69 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 205308 bases at least Q40 Consensus quality: 205701 bases at least Q30 Consensus quality: 205890 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0814I21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WUGSC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
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71051. .206235
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35622 c 35547 g 64839 t
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71050: gap of unknown length
206235: contig of 135185 bp in length
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This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (18-OCT-2001) Department of
Submitted (18-OCT-2001) Department of
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Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                  once,
                                                                                   NOTICE: This sequ
It may be shorter
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUN-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA 7. (bases 1 to 49623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-DEC-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                 On Feb 16, 20 Submitted by:
                                                                                                                                                                                                                                                                                                                        University, Genome Sequencing Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                            or longer because we provide poring submissions.
                                                                                                                                                                     Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
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                                                                                                                                               rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                           because we only sequence overlapping sec
ecause we provide a small overlap between
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d Y92H12BR,
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4444 Forest Park Avenue,
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Missouri 63108, USA
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                                                                                     sections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mttkrvpskiviagsskitlndrfsaipkprvkatvmkaqpkrf
saqpkrfsveyeeveyvpkfmkprpkprqciqqravipiqnrvsfvnampvqrfypri
nnfvhrshqmqnnfkkpfrqnfnhqnrkmfpgnnnrfqhpkqkqfptmpakksvaeld
                                                                                                                                                                                                                              /note="coded for by the following C. elegans
yk114a10.3, yk114a10.5, yk254e10.3, yk254e10
yk337h7.5, yk605b11.3, yk605b11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translation="MNEFISWCKGRGYQFDGLEITCPPPGNCGNGIYATTGFRTGKAF
ITLPETDMINAALVVDLPVYRKKLAKIGEKLKPWILITMFFAFEDTEHSAWSPYLKV
LPKEFNTPAFKGIDYDVTLPLSIKKWIDQKKEISEISEKVYKSVTKHPIFLRFSGY
FLQKSSKKFRKIAKNFNFSPIFWFFTQKRAKKFRKIAKNSNFFRIFWVTREHEMVLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LREGCGHVDSEVADTLAYLIDRVEERSLTAQELAEKLDPELVKAVDHMNKAVAREKNA SMTSIFRNLNDFVTGFNKRRDALFEEIKKLKN"
                                                                                                                                                                                                                                                                                                                  complement(join(22391. .22562,23561. 23876. .23969,24049. .24116))
                                                                                                                                                                                                                                                                                                                                                                                      complement(22391.
                                                             RELDDYMRKPKHAPITI"
                                                                                                                                            /product="Hypothetical protein Y92H12BR.2"
/protein_id="AAK09077.1"
/db_xref="GI:12863252"
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/gene="Y92H12BR.6"
join(14267. .14887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical
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/db_xref="GI:12863254"
               /gene="Y92H12BR.3"
                                                                                                                                                                                                                                                                                                                                                              /gene="Y92H12BR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical protein Y92H12BR.6"
/protein_id="AAK09076.2"
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yk258f5.5, yk372d4.5, yk258f5.3"
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/gene="Y92H12BR.7"
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/db_xref="taxon:6239"
/chromosome="I"
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/gene="Y92H12BR.6"
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/strain="Bristol N2"
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25060, 25118. . 25283, 28534. . 29631, 31011. . 31315,
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yk337h7.3,

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                                cagcttccagaatttttagcagacattgtacaaaaacttggagggtttgtccttaaaaaa
                                                                                                                                                                                                                                                                                     TTTTTCTACTAAAATTTTGAATTTTTTGCCAAAAAATTGTTTAATTTTCCGTTAATTTA 45361
                                                                                               TTTAAATTTTTTTTTTTAATTTAGGATAAATTTGAATTTTCCGTCAGTTTTATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mSQAARSAKERALQIVEQASRIRIQDARDNIGARTTGRQLKKGH
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RLIDLGWINPPQPIDISTLCTTQKFQINPKMRQYGFDLTEEGADSFPYSIDIEVQYAT
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STVALNHVSVBLDRYELPVGIBDAVVHGVWCKRRNDTVLVLKFLDEYXAILNYEDPST
STVALNHVSVBLDKYELPVGIBDAVVHGVWCKRRNDTVLVLKFLDEYXAILNYEDPST
SIRSDVVEVLYKKTKKVIHTAGDSFBKOVKLEKAFPKRYKNGTDYILHDEVXYSFETMS
HGACQSFSPLDDSSEDVLVKNGTDHFIMNNMEWLLVDPGLRFSLYESDVDMVGTAFKT
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PESYKISGSMTDWMKASTSLLVESASKEFRVLEKQTRDQMPEKWIQELTGAKLTSFIN
VTSGECIGNVSKPDLFKISRFESIIGADTSSLYSIILGLIEFDKSHTGFFVEDHVEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRGYLCEEQEIEKERALSAQIRGYTLPPPPSSAALKAVDQVFHGIPSGSVVSLADRKV
FVTKNELHREYYSSRRADKLYS"
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yk257g6.5, yk344f6.5, yk440f7.3, yk440f7.5, yk454f2.5,
yk60ld9.5"
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/gene="Y92H12BR.4"
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complement/1-7
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VESRDSGLEMIVRVAEKTEKKPGNVVGYNYTTELTTAEIFKLMNDSMTLDKMPIEVLK
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/protein_id="AAK09082.1"
/db_xref="GI:12863257"
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/gene="Y92H12BR.8"
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                                                                                                                                                                                                                                                                                                                             GAAAAAGTTTTTTTAGAAATTTGCAATGAATTTGTTTTTAGTGTGTTATGGAATTTGC
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                                                     TTTCTATTTCAGTATTCAATTATGTTTCTAATTTTCAGAAGAGGAACTCCTGCTCGTTTT 35244
                                                                                   tattaaaaaatatattcattcaccattaccaagtgctgttttgcagataatggagaagat 474
                                                                                                                       TTCCCGTTAACTACAGTAATCTATCATCCCTATGTAAATTGTTTCAATCAGAGGTGTGTT
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Department of Genetics, Washington
St. Louis, MO 63110, USA
e-mail: jspieth@watson.wustl.edu
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Db 35243 ACAATCCCAGATACTGGATCAAGAA 35219

Search completed: May 22, 2002, 06:36:01 Job time: 7746 sec

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## ALIGNMENTS

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AAH20176
                                                                                                                                                                                                         Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of rethal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                       Key
                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                  AAH20176;
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20-OCT-1999;
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                                                                       WO200129266-A2
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                              abnormal neuronal lipid storage; genetic disorder; characterisation; ds
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                                                                                              "mutated spastin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purkinje cells and cabnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify subject baving or at risk of developing a disorder associated with Spastin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy and as a spastin polypeptide agonists. (I), their fra
or their complements can be useful for assaying the presence of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                        agtcattttagacgatgaatctgaagcacagcttccagaatttttagcagacattgtaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation; ds
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                              Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of purkinje cell;
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C N. B. The present sequence is not given in the present specification but is derived from the present specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
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RESULT AAH201179
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The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autosomal recessive spastic ataxia of Charlevoix-Saguenay; mu neurodegenerative disease; reduced sensory nerve conduction; reduced motor nerve velocity; hypermyelination of retinal ner atrophy of upper cerebellar vermis; absence of purkinje cell;
                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                  useful for diagnosing autoso
Charlevoix-Saguenay disease
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mal recessive spastic ataxia of Charlevoix-Saguenay; mutation;
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HOPITAL SAINTE-JUSTINE
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iagnosing autosomal recessive spastic ataxia of
aguenay disease by detecting two point mutations
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Best Loc
Matches
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Human mutated 09-AUG-2001

spastin nucleotide sequence

SEQ

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NO:15

(first entry)

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The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic attaxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in CC gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC analysis of an early onset neurodegenerative disease in an individual. CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC markers, as an antigen, identify and express recombinant protein for CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC the present invention can be used to identify subjects having or at risk of a flavoring a disease or discorder associated with abarrant expression.
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                                                                                                                                                                                                                                                                                                                                                               of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix Saguenay disease by detecting two point mutations in spastin
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                                                                                                                                                                                                                                                                                                       protein or spastin gene expression or activity. The present sequence encodes a mutated human spastin.
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WPI; 2001-308494/32.
P-PSDB; AAB97820.
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New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin gene sequence

Claim 1; Fig 8; 76pp; English.

markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with spastin protein or spastin gene expression or activity. The present sequence encodes mouse spastin as given in the present invention. chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease complements early ensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to

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8.4%; 49.3%;

Score 42.2; DB Pred. No. 0.084; Mismatches 113;

DB 21;

Length Indels

1251; 0,

Gaps 92

0

Conservative

0;

Sequence 1251 BP; 581 A; 93 C; 171 G; 406 T; 0 other,

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RESULT 7
AAA70119/c
                            P. falciparum: Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing effor vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                          Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore,
                                                                                                                                                                                                          (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins encoded by chromosome 2 of Plasmodium falciparum, useful as an diagnosis of P.falciparum infection
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(CARU/)
(GARD/)
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antimalarial; malaria;
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) CARUCCI.D.
) GARDNER M.
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                                           AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune system disorder; AIDS; autoimmune disease; rheumatoid arthr inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to human secreted proteins can also be used in alleviating symptoms associated with the disorders and i diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated
                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 32834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 38 human secrete preventing, diagnosing and/or treating disease and diabetic retinopathy -
                                      23-MAR-2001; 2001WO-US09231
                                                                                                   27-SEP-2001.
                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                      pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL12784 standard; cDNA; 3644 BP
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                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide
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                                                                                                                                                                                                                                                                                      gene;
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Best Local
                                                                                                                          Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breed 240017 region G3; 318013 region A3; 515002 region G2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                              19-JUL-2001
                                                              WO200151627-A2
                                                                                           Glycine max.
                                                                                                                                                                                     Soybean 318013 region A3, SEQ ID NO:
                                                                                                                                                                                                                                                    AA161373
                                                                                                                                                                                                                                                                                 AAI61373 standard; DNA; 513445 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 30; Page 596-893; 1353pp; English.
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Pred. No. 9.
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RESULT 13
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Best Local Similarity
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(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2081 A;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          part of the printed format directly from
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Best Local
                                              21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                               9296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation \,
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01-SEP-2000;
                                                                                                          21-MAR-2001;
                                                                                                                                                          WO200170955-A2
                                                                                                                                                                                  Streptococcus pneumoniae
                                                                                                                                                                                                          antibiotic;
                                                                                                                                                                                                                      Antisense;
                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                      13-FEB-2002
                                                                                                                                                                                                                                                                                               AAS55610
                                                                                                                                                                                                                                                                                                                     AAS55610 standard; DNA; 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11172 BP; 3178 A; 73 C;
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             16-FEB
                      27-NOV-2000;
22-DEC-2000;
                                                                                                                                   27-SEP-2001.
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77; Conserv
             2001;
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                                                                                                                                                                                                         ds; prokaryotic cellular proliferation gene;
; antibacterial; drug design.
          2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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2000DE-1043826.
                                                                                                          2001WO-US09180
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                                                                                                                                                                                                                                             pneumoniae DNA for cellular proliferation
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53.8%;
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Pred. No. 3
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

On the sequence data for this patent did not form part of the printed control of the protein.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Seq
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P-PSDB; AAU37751.
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                                                                                                                       Genomic library; bacteria; human upper airway; otitis bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                     Genomic fragment
                                                                                                                                                                                                     04-APR-2001
                                                                                                                                                                                                                                    AAF28534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2543 GATTCCTGCCAACTATAAATAGCATCTCCAAACAAACTTCCCAACTCTTTCACAAATTCA
16-JUN-2000; 2000WO-US16649.
                                                           WO200078968-A2
                                                                                       Moraxella catarrhalis
                                                                                                                      bronchopulmonary; endocarditis;
                                                                                                                                                                                                                                                               AAF28534 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3129 BP; 957 A; 533 C; 696 G; 943
                             28-DEC-2000
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Xu HH;
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                                                                                                                                                                     #21.
                                                                                                                                                                                                                                                               DNA;
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52.6%;
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Matches 81; Conserv
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                                                                         22658
22718 tccttaataaaaaatatccttaataaaaatatc 22751
                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acids -
                                                                                                                                                                                                                                                                                                          Sequence 39003 BP; 11568 A; 8751 C; 7476 G; 11208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 171-180; 545pp; English.
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                                                                                                                                                                                                                                                                                                                                                  and meningitis.
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                                                                                        351 acattgtacaaaaacttggagggtttgtccttaaaaaattagatgcatctatacaacatc 410
                                                                                                                                                              291 ttccatcgttagtcattttagacgatgaatctgaagcacagcttccagaatttttagcag 350
                  cgcttattaaaaaatatattcattcaccattacc 444
                                                                       Patterson C,
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52.68;
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Search completed: May 22, 2002, 06:43:32 Job time: 8022 sec

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Result
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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length: 2000000000
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US-08-190-687B-24
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US-08-649-046-3
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US-08-680-395-1
US-08-680-395-1
US-08-680-395-1
US-08-416-603-1
US-09-04-113-13
US-08-416-603-1
US-09-132-118-1
US-09-132-118-1
US-09-132-118-1
US-09-133-944-2
US-09-234-1861-1
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US-08-960-780-43
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29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.8	30	30.2	30.4	30.6	30.6	30.8	30.8	30.8	30.8
5.9	5.9	5.9	5. 9	5.9	5.9	5. 9	5.9	6.0	6.0	6.0	6.1	6.1	6.1	6.2	6.2	6.2	6.2
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Sequence 179, App	Sequence 179, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 15, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 105, App	Sequence 38, Appl	Sequence 33, Appl	Sequence 9, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 67, Appl

## ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: May, Earl
APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: dnaE
FILE REFERENCE: GM10237
CURRENT APPLICATION NUMBER: US/09/387,695
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3129
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-387-695-1
RESULT 2
US-09-328-111-775
US-09-328-111-775
: Sequence 775, Application US/093281
: Patent No. 6262333
: CREMERAL INFORMATION:
: APPLICANT: Endege, Wilson O.
: APPLICANT: Steinmann, Kathleen E.
: APPLICANT: Burgess, Christopher C.
: APPLICANT: Bushnell, Steven E.
: APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 80; Conserv
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51.9%; Pred. No. 0.5;
tive 0; Mismatches 74; Indels 0
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; NAME/KEY: misc_feature

; LOCATION: (1)...(658)

; OTHER INFORMATION: n = A,T,C

US-09-328-111-775
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APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GE
TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.u
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wong, G.
APPLICANT: Martin,
APPLICANT: MCCormin
APPLICANT: Rubinfe
APPLICANT: O'Rourk
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/08190687B Patent No. 5760203
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                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                 STREET: Chicago
                                                                                                                                                                                                                                          TITLE OF INVENTION: GAP Gene Sequences NUMBER OF SEQUENCES: 27
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               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                       ADDRESSEE:
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60606-6402
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O'Rourke, Edward C.
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                                                                                                                                                                                Marshall, O'Toole, Gerstein, Murray & 100 Sears Tower, 233 South Wacker Drive
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47.08;
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                                                                                                                               of America
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                   Version #1.30
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US-08-190-687B-7
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Best Local :
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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PRIOR APPLICATION DATA:
07/774,644
                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 07/774,644
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
07/260,807
                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2160 AATACTTCCACCGACATTGAGATATATTTATGGGTGTTTACAGAAATCTGTTCAGCATA 2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2100 TITAACACACCTATTGAACATACTTTCAGAGCTTGTGGAGAAAATATTCATGGCTTCAGA 2159
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LOCATION:
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STATE: Illinois
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nes 66; Conserv
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   APPLICATION NUMBER:
                                                         SOFTWARE:
                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           COUNTRY:
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5. 5760203
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McCormick, Francis P.
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Rubinfeld, Bonne-
Rubi
                                                                                                                                                                                                                                           United States of America
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US/08/190,687B
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PRIOR APPLICATION DATA:

02-FEB-1994

APPLICATION NUMBER: 07/7 FILING DATE: 11-OCT-1991

07/774,644

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Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2710 AATACTTCCACCGACATTGAGATATTTTATGGGTGTTTACAGAAATCTGTTCAGCATA 2768
                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING,
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                                                                                                                                                                                                                                                                                                               APPLICANT: OLSZEWSKI,
APPLICANT: JACOBSEN,
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
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APPLICATION NUMBER: US/0:
FILING DATE: 16-MAY-1996
CLASSIFICATION: 435
CTORNEY/AGENT INFORMATION:
                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                            STATE: MINNESOTA
                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312/474-0448
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119..3259
                                                                                                                                        Floppy disk
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                                                                                                                                                                                                                                                                                                                 IDENTIFICATION AND
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                                                    US/08/649,046
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 612-30 NO: 3
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
SERVICH: 6479 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/179,557
FILING DATE: 07-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4476 TAAAAATTAAGATTTTTATTTGGAGCACTTCCGAAAACCCAAAATTGCATCTTGAACCAAA 4417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1225
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-SEP-
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VRANG, Astrid
TITLE OF INVENTION: Recombinant Lactic Acid Bacterium
TITLE OF INVENTION: Containing an Inserted Promoter and Method of Constructing
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 accaagtgctgttttgcagataatggagaagatgccattgcagaaaattgtgtaatcaa 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/DK94/00004 FILING DATE: 03-JAN-1994
                  APPLICATION NUMBER: US 08/036,681 FILING DATE: 25-MAR-1993
                                                                                                                                                                                APPLICATION NUMBER: DK 1579/92 FILING DATE: 30-DEC-1992
                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGTACTTTTGTTTGGTATCTGGTGGATCAGCCAACGAATCTGTAATTCTGTAATCAA 4359
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5837509
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                                                                                                                                                                                                                                                                                                                                                                                                                                    r: 3000 K Street, N.W. Washington, D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADSEN, Soeren Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BECH HANSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOHANSEN, Er
NILSSON, Dan
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55.1%;
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Pred. No. 3.2;
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Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08680395 Patent No. 5892010
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Godfrey, Tony
APPLICANT: Kowbel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPAX: 202 672 5399
                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AGTCTCCATTAATTTATAACTCTATTGTAGAATTTTCTGGCTATTTAGA--TAGTAATAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
REFERENCE/DOCKET NUMBER:
                   REGISTRATION NUMBER:
                                      NAME:
                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 TATTCTTAAATATTTTGTTTTTCTAT 17
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           Pastian, Kevin L.
Bastian, Kevin L.
34,774
                                                                                                                                                                                                                                                                                California
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                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins, Colin
Hwang, Soo-in
                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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47.7%;
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                                                                                                             us/08/680,395
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023070-068900US
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Pred. No. 2
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                                                                             TELEFAX: (202) 293-78 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: (202) 293-7060
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1274 GAAGACTCATGATTTCTATTTTGAG 1299
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                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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              STRANDEDNESS:
                                                                                                                                        REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                      FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                     APPLICATION NUMBER:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                            LENGTH:
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           nucleic acid
EDNESS: single
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                                         149 base pairs
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2100 Pennsylvania
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                                                                                            293-7860
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51.4%;
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RISK OF
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transcript of tyrosine kinase 
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Avenue, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR DIAGNOSING AN INCREASED BREAST OR OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.4;
Pred. No. 4;
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US-08-759-873-4
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US-08-759-873-4
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                                                                                                                           Matches
                                                                                                                                           Query Match
Best Local
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                101 gaattgattgttcaatggtatccatttgatgaaaacagaaatca 144
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   72
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                                                                               41 aatccagaacgatttgcacgtcttatcaaggaagtaatgaatacattctggcctggcaga 100
                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 12-APRIL-1996
                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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GAAATAAGAATGATACGGTATCCATGACATGAGAACAGAAAACA 115
                                                            1 Similarity 56.7
59; Conservative
                                                                                                                           59;
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2100 Pennsylvania Avenue, N.W., Suite (
ashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kieback, Dirk G.
VENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
VENTION: OF BREAST OR OVARIAN CANCER
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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56.78;
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                                                                                                                                      Score 32; DB 1; Length 149; Pred. No. 1.8;
                                                                                                                         Mismatches
                                                                                                                         45;
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US-09-004-113-13
RESULT 11
US-08-416-603-1/c
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                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Hanna, Wayne W.
APPLICANT: Roche, Dominique
TITLE OF INVENTION: Nucleic Acid Markers for
TITLE OF INVENTION: Apospory-Specific Genomic Region
TITLE OF INVENTION: 44
                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: U12 3'end
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TELEPHONE: 301-504-5302
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NAME: Poulos, Gail E.
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LENGTH: 180 base pairs
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                                                                             173 tggaaaaa 180
                                                           146 TGTAAACA 153
                                                                                                                                        113 caatggtatccatttgatgaaaacagaaatcacccatctgtttcatggcttaagatggtt 172
                                                                                                                     86
                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                ORGANISM: Pennisetum squamulatum
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Poulos, Gail E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                     CAATTGAATTTTTTCAAAAATACCAACAACCAAATCTTTTGATCTTCTGGTGATGGTA 145
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Beltsville
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SYSTEM: PC-DOS/MS-DOS
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53.1%;
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                                                                                                                                                                                                                                          60;
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Sequence 1, Application US/08416603 Patent No. 5866780

NUMBER OF SEQUENCES: 1

ADDRESSEE:

APPLICANT: Reddick, Bradford B.
TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and
TITLE OF INVENTION: Uses Therefor

APPLICANT:

Reddick,

Law, Marcus Hebara, Ledare

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NAME: Lloyd, Jeffrey
REGISTRATION NUMBER: 35,589
TELECOMMUNICATION INFORMATION:
TELECHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                              Patent No. 5691185
GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                     APPLICANT:
NUMBER OF SEQUENCES:
                TITLE OF INVENTION:
                           TITLE OF INVENTION:
                                                                                                APPLICANT: DICKELY, Francoise APPLICANT: JOHANSEN, Eric
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                                                         APPLICANT:
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LOCATION: 435..10763
OTHER INFORMATION: //
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                                                                                                                                                                                                                                  GTACGAATCCCCTAATAGTTTACT
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                                                                                                                                                         Application US/08242098
                                                                  JOHANSEN, Eric
NILSSON, Dan
HANSEN, Egon
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2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                      STROMAN, Per
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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            Lactic Acid Bacterial Suppressor Mutants and Their Use as Selective Markers and a Containment in Lactic Acid Bacteria
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Pred. No.
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Best Local Similarity
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ZIP: 20007-51,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Tipm PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Toronsyms-bos
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                                                                                                                        TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: qn4176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707
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                COUNTRY:
ZIP: 940
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                                           STATE:
                                                          CITY: HILLSBOROUGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGACCTTGAAGAGGCTGATGGAAAAGCAACAATTACGCTTTATGGTAAATCAGCGCATG 826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                           CALIFORNIA
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                                                                          2: SCIENCE & TEO
                                                                                                                                                                                   HSU, HAILING
GOEDDEL, DAVID V
                                                                                                                                                                                                                     HUANG,
                                                                                                                                                                                                                                     BAICHWAL, VIJAY R
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52.78;
                                                                                                                                       RIP: NOVEL HUMAN PROTEIN INVOLVED TUMOR NECROSIS FACTOR SIGNAL TRANS ASSAYS
                                                                                           & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/133,390
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Pred. No. 4.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:

Release #1.0, Version #1.30

MEDIUM TYPE:

Floppy disk

APPLICATION NUMBER:

US/09/132,118

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Query Match
Best Local Similarity
"atches 67; Conserve
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; LOCATION:
US-09-132-118-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-3341
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                       APPLICANT:
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,511
                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 atggag 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                     952 ATGCAG 957
                                                                                                                                               ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                            OPERATING SYSTEM:
                                                             COMPUTER:
                                                                                                                     COUNTRY:
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19103-2793
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Ward, Judith
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                                                          IBM Compatible
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53.2%;
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Pred. No. 5.9;
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/011
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: PCT/US
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: PCT/US
FILING DATE: 19-FEB-1997
APPLICATION TO THE TOTAL NUMBER: PCT/US
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 215/994-2252
                   ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1557 ACGCCGTAATCCATACTCAGTCATTCTATTTGATGAAATCGAAAAAAGCAAATCCACAAAT 1616
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CELL DEATH PROTEIN NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lee, Tae-Ho
APPLICANT: Kim, Emily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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STREET: Δ.

TTTY: Boston

VA
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                                                                                                                                                                                                                                                                                 COUNTRY:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215/994-2222
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                                                                                            CLASSIFICATION:
                                                                                                                    FILING DATE:
                                                                                                                                   APPLICATION NUMBER:
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Seed, Brian
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Pred. No. 6;
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENDESS: single
TOPOLOGY: linear
NO.ECULE TYPE: DNA
US-08-444-005-16

Query Match
Best Local Similarity 53.2%; pred. No. 6.1;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
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Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
Matches 67: Conservative 0; Mismatches 59; Indels 0; Gaps 0;
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Mismatches 59; Indels 0; Gaps 0;
Mismatches 59; Indels 0; Gaps 0;
Mismatches 59; Indels 0; Gaps 0;
Mismatches 59; Indels 0; Gaps 0;
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Mismatches 59; Indels 0; Gap
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Perfect score:
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396.6
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43.8
41.4
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic search, using sw model
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Match
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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gb_htc:*
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BAZ644393

BH110525

BH2644393

BH26440G

CNS0440G

BE597419

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AZ066617

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AZ247902

CNS00DDH
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1864.535 Million cell updates/sec
               BH025017 RPCI-24-3
BH126217 RPCI-24-3
AZ649875 IM0510B14
BE008891 CM4-BN016
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AZ547902 ENTDP11TF
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AUTHORS
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 318 row: E column: 15
Seq.primer: SP6
Class.
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Other_GSSs: RPCI-24-318E15.TVB
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Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
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BH146623 ENTPZ7TR
AZ611614 1M0438J01
AZ660635 1M0538014
AZ528035 ENTC142TF
AL104456 Drosophil
BB523933 BB52393
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BH256414 KG00869 D
BH155613 ENTSX92TR
AL063921 Drosophil
BF709704 MI-P-AY0-
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Levins, M.,

BAC end

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RESULT 2
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AUTHORS
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ORGANISM
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Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
Other GSSs: RPCI-24 318C15.TVB
Contact:,Shaying Zhao
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae 1 (bases 1 to 796)
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Pred. No. 6.7e-94;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 318 row: C column: 15
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CAGAAGTTGTGTAATCAAA
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Class: BAC ends
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/clone_lib="RPCI-24"
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1M0519B14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0519B14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0519 row: B column: 14
Seq primer: CACACAGGAAACAGCTATGACC
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1 (bases 1 to 558)
Dunn, D., Aoyagi, A.,
Islam u
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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Mammalia; Eutheria; Rodentia;
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                                                                                            Similarity 84. 97; Conservative
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                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0519B14"
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/strain="C57BL/6J"
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-TTGGAAGAATCTCTATATACATTTCTCAGAAGATTTG 56
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                                                                                                                                                                                                                                                                                                                              High quality sequence start: 6
High quality sequence stop: 241.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl7tl-&t2-CM4-BN0161-040
400-132-d08&t3=2000-04-04&t4-1)
Seq.primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Dias Neto, E., Garci
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      വ
                                                                                    /note-"Organ: breast_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification low stringency conditions."
40 c 47 g 81 t
                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0161"
/dev_stage="Adult"
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Best Local Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0508 row: M column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were
                                                                                            /lab_host="p. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0508M18"
                                                                                                                                                                                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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Pred. No. 1.4e-45
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                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 340 row: G column: 10
                                                                                                                                                                                                                                                   Other GSS: .... Contact: Shaying Zhao Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence.
BH110525
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Other_GSSs: RPCI-24-340G10.TV
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                    Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                 9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.6e-32;
Pred. No. 1.6e-32;
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source

/organism="Mus musculus"

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RESULT 7
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                          Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS;
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110L02 of
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                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS; genome survey sequence. 
Tetraodon nigroviridis.
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                                                                                                                                                                                                                                                                                                                               (bases 1 to 883)
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                                                                                                                   Submission
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 bp DNA linear GSS; nigroviridis genome survey sequence T7 end of clibrary G from Tetraodon nigroviridis, genomic
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/clone_lib="RPCI-24"
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/db_xref="taxon:10090"
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                                                        RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Saito, H., Sakai, C., Sagabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Shiraki, T., Tominaga, M., Toya, T., Tsnnoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al.)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                     Contact: Yoshihide Hayashizaki
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Pred. No. 7e-27;
D; Mismatches 160
Exploration
   Research
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BF397419 170 bp mRNA UI-R-BS2-bel-b-03-0-UI.S1 UI-R-BS2 Rattus UI-R-BS2-bel-b-03-0-UI 3', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="olfactory brain"
/dev_stage="10 days neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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75.2%;
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                                                                                                                                                          CACTGCAGAAGTTGTGTAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mooares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized embryo at 13 dpc library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
MR0\text{-}AN0083\text{-}160900\text{-}003\text{-}d10 AN00\hat{B}3 Homo sapiens cDNA, BF326199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
                                          BF326199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97044477
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Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="embryonic 13 dpc"
/dev_stage="embryonic 13 dpc"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D+Pac (Pharmacia) with a modified
/note="Vector: pT73D+Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BS2
library is a subtracted library derived from 13 dpc whole
embryo tissue. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soares, MB
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TAG_TISSUE=embryo at 13 dpc
TAG_SEQ=AATCC"
1 29 c 31 g 67 t
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/clone="UI-R-BS2-bel-b-03-0-UI"
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                       mRNA sequence
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RESULT 11
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BH571801
BH571801.1
                                                             Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                           BH571801
BOHLS54TR BOHL Brassica
                                                                                                                                           Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRO&t2=MRO-ANOO83-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 266)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                       UMO.T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simpson, A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160900-003-d10&t3=2000-09-16&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 11.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
(bases 1 to 752)

(bases 1 to 752)

wn,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: amnion_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="AN0083"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                            GI:17823640
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                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57;
Pred. No.
                                                                                                                                                                                                                             752 bp
oleracea
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. 0.00012;
ches 0;
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genomic clone
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one BOHLS54,
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RESULT 12
AZ066617/c
                                                  REFERENCE
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ORIGIN
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Best Local
                                                                                                    ORGANISM
                                 AUTHORS
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                                                                                                                                                                                                                                                                                                            106
                                                                                                                                                                                                                                                                                                                                            484 gaaa 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ttatatacatttttcagaggatttgactttatttgatgagatgccacttatccccagaac 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acttggagggtttgtccttaaaaaattagatgcatctatacaacatccgcttattaaaaa 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTETATGTTAATTTTTTTTTTTTGGTAAACTTTTTAAAATATGGTAATAATTCATATATT
                                                                                                                                                                                                                                                                                                          GAAA 103
                                                                                                                                                                                                                                                                                                                                                                              AAATTATAAAATTTAATCGTAAAATCATTATTTTCTCTCTGTTGACGGCGGACGATTAAA 107
                                                                                                                                                                                                                                                                                                                                                                                                           atatattcattcaccattaccaagtgctgttttgcagataatggagaagatgccattgca 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTAAAATAATATTCAAATATGACATTATAAATTTCGAAATATAATTTAATTATAT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cattttagacgatgaatctgaagcacagcttccagaatttttagcagacattgtacaaaa 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tatactagaggaaggtcagacatgtgtggaactcattagactcaggattccatcgttagt 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTTTAAATTATACAATTTTATAACTAAAATTTTCAAAAATGCATACAATTTTTTTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax:
                Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,F
                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 440)
                                                                                                  Mus musculus
                                                                                                                                      GSS
                                                                                                                                                AZ066617
AZ066617.1 GI:7357869
                                                                                                                                                                                      DNA sequence.
                                                                                                                                                                                                      AZ066617
RPCI-23-433L3.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Other_GSSs: BOHLS54TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: sheared ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Chris
and Fraser, C.M.
                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="BOHL"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
114 c 109 g 262 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHLS54"
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1. .752
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45.1%;
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Pred. No. 0.41;
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                                                                                                                                                                                                        musculus
                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                Geer, K.,
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                                                                                                                                                                                                                      linear
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                              Shatsman, S.,
                Krol, M.,
                                                                                                                                                                                                      GSS 30-MAR-2000
RPCI-23-433L3,
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REFERENCE
AUTHORS
TITLE
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VERSION
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BH131081/c
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JOURNAL
                                                                                                                                                                                                                                                                                                                             ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 AGTGATATTTTGCAGATAATGGAGAAGATACCTCTACAGAAGTTGTGTAATCAAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                               Unpublished (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agtgctgttttgcagataatggagaagatgccattgcagaaattgtgtaatcaaa 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                             1 (bases 1 to 895)
Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                    Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 433 row: L column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-433L3.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                   genomic, DNA sequence.
BH131081
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH131081 895 bp
ENTOP16TF Entamoeba histolytica
DNALibrary
                    Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                          Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                               BH131081.1 GI:15089550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "74 c 73 g 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-433L3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-23"
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87.3%;
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Pred. No. 0.4;
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                                                                                                            20850,
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ba histolytica
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Best Local Sim
Matches 102;
                                                                                                                                                                                                                                          AUTHORS
TITLE
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                                                                                                                                                                                            Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 896)

Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Ent HM1:IMSS sheared DNA library (2001)
Unpublished (2001)
                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                       genomic, DNA sequence.
BH136596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH136596 896 bp DNA ENTNC65TF Entamoeba histolytica Sheared
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                                                                Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica.
Entamoeba histolytica
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                                                                                                                                                                            Contact: Brendan J Loftus
                       Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                         Email: bjloftus@tigr.org
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library
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/note="Vector: pHOS1; Site_l: Bst i; Constructed at The
/note="Vector: pHOS1; Site_l: Bst i; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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117 c 103 g 373 t
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50.2%;
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Pred. No. 2.
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JOURNAL COMMENT
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                                                                                                                                                                                                                                AUTHORS
TITLE
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Best Local Similarity 50.2%;
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High quality sequence stop: 723
Location/Qualifiers
                                                                                                                                                                              Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 940)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1:IMSS sheared DNA library

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                       940 bp ENTDP11TF Entamoeba histolytica genomic, DNA secure
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                                            Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                 genomic, DNA sequence. AZ547902
                                                                                                                                                                                                                                                                                                                        Entamoeba histolytica.
Entamoeba histolytica
    Email: bjloftus@tigr.org
Clones are derived from :
                                                                                                                                                                                                                                                                                                                                                                                            AZ547902.1 GI:11170987
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
using a method described by Clark and Diamond (Clark,
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/db_xref="taxon:5759"
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the Entamoeba histolytica HM1:IMSS sheared
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ba histolytica
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Best Local Similarity 50.2%;
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ACAATTAATAAAAAGTTACTTAT 685
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High quality sequence stop: 873.
Location/Qualifiers
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/note="Yector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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92 c 149 g 306 t
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/strain="HM1:IMSS"
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 41.4; DB 12;
Pred. No. 2.1;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 940;
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Search completed: May 22, Job time: 4071 sec 2002, 05:31:11

OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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   Score
                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Query
Match Length DB
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Gapop 10.0 , Gapext 1.0
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20
1 gtgaatggccactttgcact 20
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AC09339 AC01597 AL62677 AC09339	AC0794 AC0794 AC0794 AC07946 AC06789 AC09760		AXII 1993 AF11935 AF11335 AF11335 AF11335 AF000907 AP000126 AP00127 AP009507 AP009507 AP009507 AP009507 AP009507 AP009507 AP009507 AP009507 AP009507 AP009507 AP009507	
597 597 677 339	07/8821 HOMO 0663043 Mus n 007907 Homo 079465 Homo 067893 Homo 097609 Rattu	101171 Mus mu 101171 Mus mu 003251 Oryza 094213 Rattus L592547 Mouse 092265 Homo s 092265 Human	119933 Sequility	9931 Sequen 3556 Homo s 7766 Human 9761 Homo s

## ALIGNMENTS

ORIGIN	BASE COUNT			source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX119931	RESULT 1
	4163 a 2256 c 2487 g 3887 t	/db_xref="taxon:9606"	/organism="Homo sapiens"	112793	Location/Qualifiers	MCGILL UNIVERSITY (CA) ; Hopital Sainte-Justine (CA)	Patent: WO 0129266-A 1 26-APR-2001;	Identification of arsacs mutations and methods of use therefor	Hudson, T.J., Engert, J. and Richter, A.	1 (bases 1 to 12793)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX119931.1 GI:14036678	AX119931	Sequence 1 from Patent WO0129266.	AX119931 12793 bp DNA linear PAT 11-MAY-2001		

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SOURCE
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AF193556
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Matches 20; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital, 1650 Cedar Ave., Montreal, QC H3G 1A4, Canada Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Bouchard, J.P., Mathleu, J., Melancon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A. ARSACS, a spastic ataxia common in northeastern Quebec,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by mutations in a new gene encoding an 11.5-kb ORF Nat. Genet. 24 (2), 120-125 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens sacsin (SACS) gene, complete AF193556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engert, J.C., Berube, P.,
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                                                                                                                                                                                                         NPNVLEWLTPLKFIQISQEQMVSAGELFDPDIEVLKDLFCNEEGTYFPFSVFTSPDIL
HSLRQIGLKNERSLKEKDVVQVAKKIEALQVGACPDQDVLLKAKTLLLVUNKNHTLL
QSSEGKMTLKKIKWPFACKERPPYFGSLVMKGDLCNLCAPPDMCDVGHALILIGSSED
LVESIHVNLEKALGIFTKPSLSAVLKHFKIVVDMYSSKTFSDEDYYQFQHILLEIYGF
                                                                   WLKVPCLSTRLINPENNGFEQSGQREPLTVRIKNILEEYPSVSDIFKELLONADDANA
TECSFLIDMRRNMDIRENLLDPGMAACHGPALWSFNNSQFSDSDFVNITRLGESLKRG
EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMFDPNINHISKHIKDKSNPGIKINWSK
                                                                                                                                        MHDHLNEGKDSFRALKFPWVWTGKKFCPLAQAVIKPIHDLDLQPYLHNVPKTMAKFHQ
LFKVCGSIEELTSDHISMVIQKIYLKSDQDLSEQESKQNLHLMLNIIRWLYSNQIPAS
PNTPVPIHHSKNPSKLIMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE
                                                                                                                                                                                                                                                                                                 KKLDASIQHPLIKKYIHSPLPSAVLQIMEKMPLQKLCNQITSLLPTHKDALRKFLASL
TDSSEKEKRIIQELAIFKRINHSSDQGISSYTKLKGCKVLHHTAKLPADLRLSISVID
SSDEATIRLANMLKIEQLKTTSCLKLVLKDIENAFYSHEEVTQLMLWVLENLSSLKNE
                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF31262.1"
/db_xref="GI:6907042"
/translation="MNTFWPCRELIVQWYPFDENRNHPSVSWLKMVWKNLYIHFSEDL/TLFDEMPLIPRILEEGGTCVELIRLRIPSLVILDDESEAQLEEFLADIVQKLGGFVL
NTADIYSLVDEFSLCGHRLIIFTQSVKSMYLKYLKIEETNPSLAQDTVIIKKKSCSSK
ALNTPVLSVLKEAAKLMKTCSSSNKKLPSDEPKSSCILQITVEEFHHVFRRIADLQSP
                                               QQKRLRKFPNQFKPFIDVFGCQLPLTVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SACS"
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77. .11566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="molecular chaperone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="sacsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SACS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="sacsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="13"
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2.7;
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GKLPCRLOQTNIKLFHSIKLLVDYCFKOAEENEIEVEGLPLITILDSVLOTFDAKRRK
FLTTYHELIPSRKOLFMNTLYLKYSNILLICKYAKVFDISSFADILSSVLPREYKTKS
CTKWKONEASEEWLKNAMHFISESVSVKKDQEETKPTFDLVVDTLKDWALLPGTKFTV
SANQLVVPEGDVLLPISSIMHIAVFNAQSDKVFHALMKAGCIQLALNKICSKDSAFVP
LLSCHTANIESPTSILKALHYAWQTSTFRAEKLVENDEBALLMYENCULMHLWGODDI
KILKSLPCYKSISGRYVSIGKFGTCYVLTKSIPSAEVLEMTQSSSAFLEEKIHLKEL
YEVIGCVPVDDLLEVILKHLLPRIENLSYDAKLEHLIYLKRILSSAEELSEIKEQLEEK
LESLILIHDANSRLKQAKHFYDRTVRVEEVMLPEKLFIPODFFKKLEQLIFVKNHVTF
MTSWVEFLRNIGLKYILSQOQLLQFAKEISVRANTENWSKETLQNTVDILLHHIFQER
MDLLSGNFLKELSILFELGYERAPAEFIRFPQVQEVNGTLPLIKFNAQAVNFKFRQC
DVLQLLMTSCPILPEKATPLSIKEQEGSDLFOVEDLEGVLEWAVEDGWKLLKEEE
VVINLEYESDFKPYLYKLPLEIGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ
VVINLEYESDFKPYLYKLPLEIGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ
VUNNLEYESDFKPYLYKLPLEIGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ
VONNMETTERUNGTEREF
QKIEEYSQUALLA ACIIIKLENFMQQKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDPNEMRTVKRVYSGLFRSLQNDSVKVRSDLENVRDLALYLPSQDGRLVKSSILVFDD APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRERRLLSSILEEQLDE ETFXVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDAFLANEEKAIRLCKALREGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGHAVILLYIQHSDSKDINFLL ALAMTLKSATDNLISDTSYLIAMLGCNDIYRIGEKLDSLGVKYDSSEPSKLELPMPGT
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LYTAEHQDIVCLLQPILMENSHSFRGCGSVSLAVKEFLGLLKKFVDLLVINQLKEVAK
SVDDGITLYQENITHACYKYLHEALMQNEITKMSIIDKLKFFSFILVENAVYDSEKVS
FHLNFERAPYLVQLPNKYKNHFRELFETVGVROSCTVEDFALVLESIDQERGTKQITE
ENFQLCRRIISEGIWSLIREKKQEFCEKNYGKILLPDYNLMLLPAKSLCYNDCPWIKV
KDTTVKYCHADIPREVAVKLGAVPKRHKALERYASNVCFTTLGTEFGQKEKLTSRIKS
ILMAYPSEKEMLKELLQNADDAKATEICFVFDDRQHPVDRIFDDXWAFLQGFALCVYN
NQPFTEDDVRGIQNLGKGTKEGNPYKTGQYGIGFNSYYHITDCPSFISGNDLICIFDP
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ELRDPLMIFVLNEKVDEFSGVLRVTPCIPCSLEGHPLVLPSRLIHPEGRVAKLFDIKD
GRFPYGSTQDYLNPIILIKLVQLGMAKDDILMDDMLERAVSVAEINKSDHVAACLRSS
                                                                                                                                                                                                                                                                                       SIPPLFSGRESHKTSSKHQSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRRL
YLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSD
                                                                                                                       QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT
                                                                                                                                                                                                                                         KYSFQRFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD
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DFSVICQGFYEDIAHGKGKELTKVFSDGSTWYSMKNVRFLDDSILKRRDVGSAAFKIF
                                                                                                                                                                                                                                                                                                                                                                                                   NSSFLGKTYQIDIGYSEYKIVSSLDLYKFSRPEESSQSRDSAPSTPTSPTEFLTPGLR
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RESULT 3 AL157766/c 밁 Š DEFINITION SOURCE KEYWORDS VERSION ACCESSION cus Query Match Best Local s Matches 20 ORGANISM 6473 <u>\_</u> Human DNA sequence from clone RP1 13q12.11-12.2, complete sequence. AL157766 AL157766.9 GI:13620292 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 92693) Homo sapiens HTG AL157766 human. Similarity Conservative 100.0%; 0; 92693 bp .... ~1one RP11-40020 on Score 20; [Pred. No. 2. Mismatches DB 9 0, Length 12793; linear Indels chromosome PRI 11-APR-2001 0 Gaps

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REFERENCE

ORIGIN

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FEATURES
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emst. EMBL; Sw., cartespoor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-760M1 is at 92594 in this sequence. The true right end of clone RP11-72P19 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping Group. Further information can be round at http://www.sanger.ac.uk/HGP/Chr13 RP11-40020 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 12, 2001 this sequence version replaced gi:12709868.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
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                                                                                                                                                                                                                                                                                                                                                                                     /note="MER46A repeat: matches 1. .235 of consensus" 20613. .20912
                                                                                                                                                                                                                                                                                                                                                                                                                                          19644. .19873
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                                                                                  26938.
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/note="L2_repeat: matches 2356.
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/note="Alux repeat: matches 3.
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/clone_lib="RPCI-11.1"
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/db_xref="taxon:9606"
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/note="L2 repeat: matches 1063. .1644 of consensus"
                                                  /note="MIR repeat: matches 3. .175 of consensus"
                                                                                                                                                 /note="L2 repeat: matches 2601.
                                                                                                                                                                                                                                                      note="L2 repeat: matches 2554.
                                                                                                                                                                                                                                                                                                        note="AluSg1 repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                        note="AluSg1 repeat: matches 1. .300 of consensus"
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note="MER46C repeat: matches 1, .286 of consensus"
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/note="AluY repeat: matches 1129 of consensus" 6233062363	at_region
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e="L2 repeat: matches 25812696 of con 862187	at_region
Ote="Aludo repeat: matches 85299 of consensus	at_region
992. 60223	at_region
00te="24 copies 2 mer ca 93% conserved" 350. :59533	at_region
te="MIR repeat: matches 2153 of 6458611	at_region
te="MIR repeat: matches 82262 of consensu	at_region
e="9 copies 4 mer gaga 91% conser 357930	t_reg
te="30 co 575739	t_regio
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TO . 47873 of consensus  7747873 of consensus  1747873 of consensus	at_region
6747365	at_region
te="Alur repeat: matches 1 .307 of consensus	at_region
9946206	at_region
5145312	at_region
te="Alusq repeat: matches 1246 of consens 9045101 te="Alusq repeat: matches 1 313 of consens	at_region
triction digest data." 41. 41788	at_region
2241405 repeat: matches 1292 of consens	_feature
ore="Alusq repeat: matches 1292 of consensus 44440733	at_region
126. 40416	at_region
ote="AluSq repeat: matches 1306 or consensus 79040093	at_region
ote="AluSq repeat: matches 9301 of consensus 70339008	at_region
ote="MIR repeat: matches 22262 of consensus" 96338254	at_region
Sx repeat: matches 1308 of consensu	at_region
ote="L1ME3A repeat: matches 57876164 of cons 09836415	Ē
e="THE1B repeat: matches 1364 of conse 729834	at_region
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 Submitted
             2 (bases 1 to 99819) Waterston, R.H. Direct Submission
                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             99819 bp DNA linear Homo sapiens chromosome UNK clone RP11-143G17, *** PROGRESS ***, 44 unordered pieces
                                              Unpublished
                                                                      1 (bases 1 to 99819)
Waterston, R.H.
                                                                                                                                               HTG; HTGS_PHASE1.
                                                           The sequence of Homo sapiens
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66371. 667
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71279. .714)
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65725..6
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/note="MER31-internal repeat: matches 883..1261 o
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/note="TIGGER1 repeat: matches
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/note="TiGGER1 repeat: matches 1586. .1787 of consensus" 62566. .62865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER31A repeat: matches 47. .485 of consensus" 71780. .72075
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(10-SEP-2000) Genome Sequencing Center, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MER31-internal repeat: matches 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSx repeat: matches 1. .295 of consensus"
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70957. .71267
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SEQUENCING IN
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Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
 30994
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KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION RESULT 4 AC079761/c LOCUS

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Matches Query Match

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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 11492)
                                                                                                                         Hudson,T.J., Engert,J. and Richter,A.
Identification of areacs mutations and methods of use
Patent: Wo 0129266-A 3 26-APR-2001;
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)
Location/Qualifiers
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ORGANISM
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VERSION
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AF193557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 11493)
Engert,J.C., Berube,P., Mercier,J., Dore,C., Lepage,P., Ge,B., Bouchard,J.P., Mathieu,J., Melancon,S.B., Schalling,M., Lander,E.S., Morgan,K., Hudson,T.J. and Richter,A. ARSACS, a spastic ataxia common in northeastern Quebec, is caused by mutations in a new gene encoding an 11.5-kb ORF Nat. Genet. 24 (2), 120-125 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-OCT-1999) Genome Centre, 1650 Cedar Ave., Montreal, QC H3G 1A4, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus sacsin gene, complete AF193557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engert,J.C.,
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TECSFMIDMRRNMDIRENLLDFGMAACHGPALMSFENDSPLNITTLGESLKRG
EVDRVGKFGLGFNSVHITDIP II IMSREFMIMFDPNIMISKHIKDRSMPGIKIMWSK
EVDRVGKFGLGFNSVHITDIP II MSRREFMIMFDPNIMISKHIKDRSMPGIKIMWSK
QOKRLRKFPNQFKPFIDVFGCQLPLAVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHDHLSEGKDSFKALKFPWVWTGKNFCPLAQAVIKPTHDLDLQPYLYNVPKTMAKFHQ
LFKACGSIEELTSDHISMVIQKVYLKSDQELSEEESKQNLHLMLNIMRWLYSNQIPAS
PNTPVPIYHSRNPSKLVMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSNYLDWLMPLKFIHMSQGHVVAAGDLFDPDIEVLRDLFYNEEEACFPPTIFTSPDIL
HSLRQIGLKNESSLKEKDVVQVARKIEALQVSSCQNQDVIMKKATLLLVUNKNQTLL
QSSEGKMALKKIKWPACKERPPNYFGSLYWKODLCNLCAPPDMCDAAHAVLVGSSLL
LVESVHVNLEQALSIFTKPTINAVLKHFKTVVDMYTSKTFSDEDYYQFQHILLEIYGF
SVDDGITLYQENITNACYKYLHEAVLQNEMAKATIIEKLKPFCFILVENVYVESEKVS
                                                                                      ELRDPLMNFVLNEKLDEFSGILRVTPCVPCSLEGHPLVLPSRLIHPEGRVAKLFDTKD
GRFPYGSTQDYLNPIILIKLVQLGMAKDDILWDDMLERAESVAEINKSDHAAACLRSS
                                                                                                                                                RRLGLVPCGAVGVLLHETQEQKWTVKPHIĞEVFCYLPLRIKTGLPIHINGCFAVTSNR
KEINKTDTKGRWNTTEWRHVIVKAYLQALSVLKDLAIGGELTDYTYYAWNDDDLVHD
DFSVICKGFVEDIAHGKRELTRVFSDOSMWSMKNVRFLDDSILQRKDVGSAAPKI
LKYLKKTGSKNLCAVELPSSVKAGFEEAGCKQILLENTFSEKQFFSEVFFPNIQEIEA
                                                                                                                                                                                                                                                                          NTADIYSLVDEFSLCGHRLIIFTQSVNSMYLKYLKIEETNPSLAQDTIIIKKKVCPSK
ALNAPVLSVLKEAAKLMKTCSSSNKKLPTDVPKSSCILQITVEEFHHVFRRIADLQSP
LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTVDCTTWLICTCMDTGEALKFSLNESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSDEATIRLANMLKIEKLKTTSCLKFVLKDIGNAFYTQEEVTQLMLWILENLSSLKNE
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TDTSEKEKRIIQELTIFKRINHSSDQGISSYTKLKGCKVLDHTAKLPTDLRLSVSVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNTFWPGRELVVQWYPFSEDKRHPSLSWLKMVWKNLYIHFSEDL
TLFDEMPLIPRTLLNEDQTCVELIRLRIPSVVILDDETEAQLPEFLADIVQKLGGIVI
                         ILLSLIDEKLKIKDPRAKDFAAKYQTIPFLPFLTKPAGFSLEWKGNSFKPETMFAATE
IYTAEYQDIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKQVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF31263.1"
/db_xref="GI:6907044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="molecular chaperone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="sacsin"
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Canada
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ORIGIN

BASE COUNT

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

Tel: 4157259687 Fax: 4157259689

Email: myers@shgc.stanford.edu

RESULT G37224

DEFINITION

ACCESSION LOCUS 밁 Ş

Matches

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VERSION
KEYWORDS
SOURCE
ORGANISM
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Best Local :
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SHGC-57260
G37224
G37224.1
STS.
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medic
Department of Genetics, M-344, Stan
                                                                                                                                                  Unpublished
                                                                                                                                                                        Myers,R.M.
Human STSs (1997)
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                Homo sapiens
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KILKSLECYKSIGGYMAIJAKFGTGYVITKSIPSAEVEKWTQSSSSAFLEEKVHLKEL
KEVLGCYPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLASIEBPSEIKBOLFEK
LESLIIHDANNRLKQAKHFYDRYVFEWHJEKLFIVEKFFKKLDOYIVEKKOQAF
MTSWYEFIRNIGLKYALSGQQLLQFAKEISVRAMTENMSKETLQSTVDILLHHIFQER
MTSWYEFIRNIGLKYALSGQQLLQFAKEISVRAMTENMSKETLQSTVDILLHHIFQER
MDLLSGNFLKELSIIPFLCPERAPAEYIRFHQQYDEVKGTLPJLKFNQAQVNPEKFKQC
DVIQLLWTSCPILPEKATPLSIKEQEGSDLAPQQDLAVGTLANLINVNLDPPLDKVINNC
RNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFOLRGVAFVMVEDGWKLLKPEE
VVINLEYEADFKYLYKLPLEIGTFHQLFKHLGTEDIISTKQYVEVLSRIFKSSEGKQ
LDPNEMRTVKRVVSGLFKSLQNDSYKVRSDLFKHLGTEDIISTKQYVEVLSSILEEQLDE
APHYKSRIQGNIGVQMLYDLSGCYLGKOHGFHTKLIMLFPQKLARPLLSSILEEQLDE
ETFKVCQFFGALGSLQGLLSSEQFTGGLRIKHENDNAFLANEEKAIRLCKALR
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GKLPCROOTNLKLFHSLKLLVDYCFKDAEESBEFVEGLPLLITLDSVLOIFDGKRPK
FLTTYHELIPSRKDLFMNTLYLKYSSVLLNCKVAKVFDLSFADLLSFARVLLPRTYKFK
CAKWKDNFASESWLKNNAMFISESVSVTDDQEEPKPAFDVIVDILKDMALLPGTKFTV
STSQLVVPEGDVLIPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSALVP
LLSCHTANIDSPASILKAVHYMVQTSTFRTEKLMENDFEALLMYFNCNLSHLMSQDDI
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PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY
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ALAMTLKSATDNLISDTSYLIAMLGCNDIYRISEKLDSLGVKYDSSEPSKLELPMPGT
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95.0%;
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Pred. No. 22;
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                                    of Medicine
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      Stanford,
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      CA 94305,
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|TGAATTGCCACTTTGCACT 319
                                                                                                                                            Mitochondrion Ips latidens
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Scolytidae; Ips.

1 (bases 1 to 766)
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Primer B: CARGTTTCTCCAGGATGCCA
STS size: 99
PCR Profile:
Submitted (15-DEC-1998) ESPM-Division of Insect Biology, University of California, Berkeley, 201 Wellman Hall, Berkeley, CA 94720, Location/Qualifiers
                                                                                              Cognato, A. I. and Sperling, F. A.
Phylogeny of ips DeGeer species (Coleoptera: scolytidae)
from mitochondrial cytochrome oxidase I DNA sequence
Mol. Phylogenet. Evol. 14 (3), 445-460 (2000)
                                                                                                                                                                                                                                               Ips latidens haplotype mitochondrial gene for AF113358
                                              2 (bases 1 to 766)
Cognato, A.I. and Sperling, F.A.H.
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/db_xref="taxon:9606"
/map="10"
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18; Conserv
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Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Scolytidae; Ips.
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AF113359.1
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Cognato, A.I. and Sperling, F.A.H.
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/organelle="mitochondrion"
/db_xref="taxon:102838"
/haplotype="2"
<1. .>766
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/protein_id="AAF65880.1"
/protein_id="AAF65880.1"
/db_xref="G1:7650045"
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/translation="PGFGLISHIIGQESGKKEAFGVLGMIYAMTAIGLLGFVVWAHHM
/translation="PGFGLISHIIGVETGIKLFSWMAFFHGTOISFNESSIWSIGFIFITHM
GGLTGVILANSSIDIILHDTYYVVAHFHYVLSMGAVFAIIAGLVQWFPLFTGITLNKK
YLKTHFLTMAVGVNLTFEPQHFLGLSGWPRRYSDYPDAYLLWNIISSIGSMISLISVF
YFIFILMESFSAQRKSISALNLNSSLEWLQYLPPSDH"
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/db_xref="taxon:102838"
/haplotype="1"
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/db_xref="GI:7650047"
/tanslat.ton="pef6LISHIIGOESGKKEAFGVLGMIYAMTAIGLLGFVVWAHHM
FTIGMDVDTRAYFTSATMIIAVPTGIKIFSWMATFHGTQISFNPSSIWSLGFIFLFTM
GGLIGVILANSSIDIILHDTYYVVAHFHYVLSMGAVFAIIAGLVGMFPLFTGTTKKK
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/organism="Ips latidens"
YLKTHFLTMFVGVNLTFFPQHFLGLSGMPRRYSDYPDAYLLWNIISSIGSMISLISVF
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/transl_table=5
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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1. .9697
                                                                      /db_xref="taxon:9606"
/chromosome="10"
/note="assembly_name:Contigl
                                                    /clone="RP11-254K3"
                                                                                                         /organism="Homo sapiens"
                                                                                                                                           Location,
                                                                                                                                    9697: contig of 9697 bp in length
9797: gap of unknown length
173309: contig of 165512 bp in lengtation/Qualifiers
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 174470 bases at least 040
Consensus quality: 174909 bases at least 030
Consensus quality: 175102 bases at least 020
Insert size: 175308; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genomecorp.com/
Contact: gtc-seqcenter@genomecorp.com
------ project Information
Center project name: hg364
                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 7.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: GTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Genome Therapeutics Corperation
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Pred. No. 71;
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ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                     RESULT 12
AP001265/c
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AUTHORS
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ORGANISM
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KEYWORDS
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AP000751
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-NOV-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RKEN), Genomic Schences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail: hattori@ssc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                 AP001265 192913 bp DNA 1i
Homo sapiens chromosome 11 clone RP11-741L23
DRAFT SEQUENCE, 34 unordered pieces.
                  HTG;
                                AP001265.2 GI:8117657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Mar 21, 2001 this sequence version Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama, A., Yada, T., Totoki, Y., Watanabe, Homo sapiens genomic DNA Published Only in DataBase (1999) In press (bases 1 to 176713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AP000751
AP000751.4 GI:13429919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens DNA,
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HTGS_PHASE1; HTGS_DRAFT.
sapiens DNA, clone:RP11-741L23.
                                                                                                                                                                                                                                                               Conservative
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9798. .175309
/note="assembly_name:Contig2
clone_end:T7"
a 36843 c 34823 g 48645 t
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33938 c 32613 g
                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 91;
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Pred. No. 91;
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                                                                                                                                                                                                                                                                                                 DВ
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map 11q24,
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Gaps

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30-MAY-2000 WORKING

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominid (bases 1 to 19291)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hor Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Homo sapiens 192,913 genomic DNA of 11q24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contigs are represented as runs N, are unknown. This record will be up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattorleysc.riken.go.jp., Juliani, Juliani,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Only in DataBase (2000) In press
2 (bases 1 to 192913)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suguencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329 Consensus quality: 170147 bases at least Q40 Consensus quality: 181282 bases at least Q30 Consensus quality: 186868 bases at least Q20 Insert size: 189613; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                  108170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 4.30x in Q20 bases; sum-of-contigs
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160241
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152973
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145327
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182703
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175015
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and Sakaki, Y.
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* arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence 
* as soon as it is available and the accession number will
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 34 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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187915
190403
191852
                                                                                                                                                    177404 177503: gap of 177504 178982: contig
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133572 139936: contig
139937 140036: gap of
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L75015 177403: cont
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120625: contig of 6635 bp in
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113890: cont
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Unpublished
              Sequence Data
                         Smith,D.R.
Genome Therapeutics Corporation Sequencing
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (31-DEC-1999) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 23, 2000 this sequence version replaced gi:7630670. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens, clone RP11-14E3
Unpublished
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                                                                                                                                                            Direct Submission
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Homo sapiens clone RP11-14E3, ***
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Pred. No. 92;
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is
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Center clone name: 14_E_3
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17689: contig of 1054 bp in 16
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2131: contig of 1553 bp in 16
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27763: gap of 100 bp
27635: gap of 100 bp
27636: contig of 1739 bp in 16
27763: gap of 100 bp
276374: contig of 1731 bp in 16
                                         38540: contig of 2063 bp in

18640: gap of 100 bp

40445: contig of 1805 bp in

10545: gap of 100 bp

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51530: gap of 100 bp

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06 94475: contig of 3170 b

76 94575: gap of 100 bp

76 96917: contig of 2342 b

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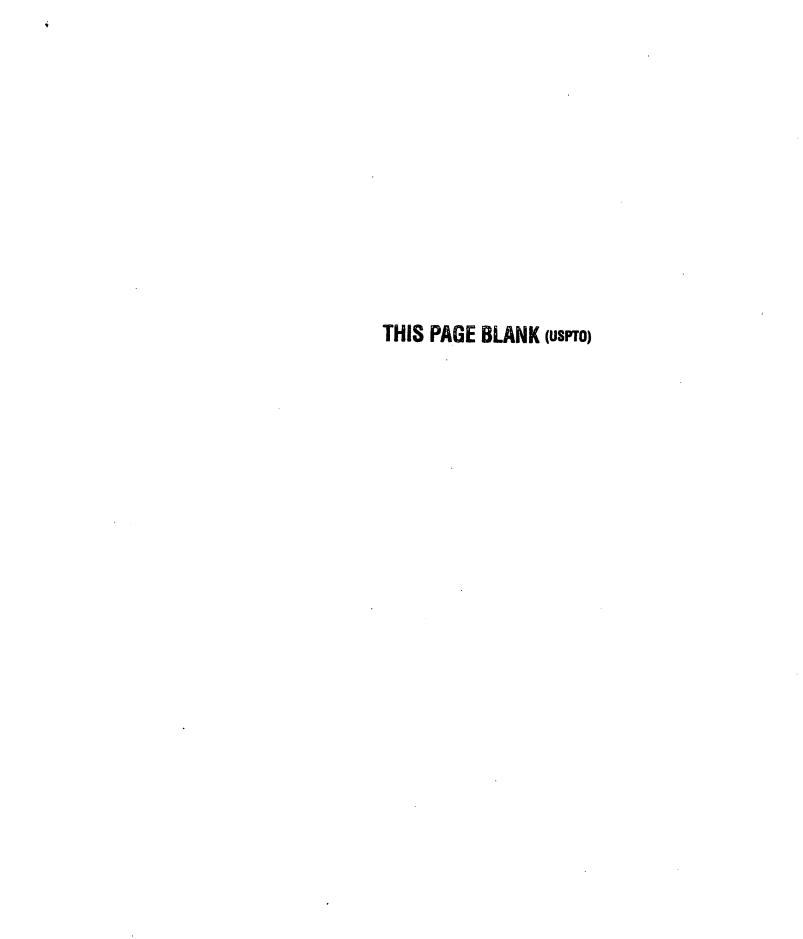
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Hrincevich,A.W., Rocha-Olivares,A. and Foltz,D.W.

Direct Submission
Submitted (02-FEB-2000) Zoology and Physiology, Louisiana State University, South Campus Drive, Baton Rouge, LA 70803-1725, USA Sequence update by submitter
On Feb 2, 2000 this sequence version replaced gi:2105417.
Location/Qualifiers
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Astero
Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae;
1 (bases 1 to 993)
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Hrincevich, A.W. and Foltz, D.W.
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198238: gap of 100 bp
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221920: gap of 100 bp
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JOURNAL MEDLINE REFERENCE AUTHORS TITLE RESULT 1
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KEYWORDS
SOURCE REFERENCE TITLE ORGANISM AUTHORS 4318 bp Homo sapiens mRNA for KIAA0730 p AB018273 AB018273.1 GI:3882180 2 (bases 1 to 4318) Ohara,O., Suyama,M., Direct Submission Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA ness 5 (5), 277-286 (1998) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Homo sapiens adult male brain cDNA to mRNA, clone\_lib:pBluescriptII SK plus clone:hk03632. (sites) Nagase, T., Ishikawa, K. and Kikuno, R p mRNA linear protein, partial cds PRI 16-JUN-1999

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ILLY1QHSDSKDINFLLALAMTLKSATDNLISDTSYLLAMLGCMDIYRIĞEKLDSLĞV
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FFVPTFKSVGNPVEARRWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAAD
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MLNVNLDPPLDKVINNCRNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRG
VAFVNVEDGWKLLKPEEVVINLEYESDFKPYLYKLPLELGTFHQLFKHLGTEDIISTK
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/protein_id="BA334450.1"
/db_xref="GI:3882181"
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/translation="VTEMTSWVEFLRNIGLKYILSQQQLLQFAKEISVRANTENWSKE
TLQNIYUDILLHHIFQERMDLLSGNFLKELSLIPFLCPERAPAEFIRFHPQYQEVNGTL
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/codon_start=1
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/clone_lib="pBluescriptII
/dev_stage="adult"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12793)
Hudson, T. J., Engert, J. and Richter, A.
Identification of arsacs mutations and methods of use therefor Patent: WO 0129266-A 1 26-APR-2001;
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)
Location, Qualifiers
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(bases 1 to 12793;
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                                                                                                                                                                              TDSSEKEKRIIOELAIFKRIHISSDOISSYTKLKGCKVLHHTAKLPADLRLSISVID
SSDEATIRLANMLKIEQLKTTSCLKLVLKDIENAFVLEHLSSIKNE
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77. .11566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ø SANQLYVPEGDYLLPLSLMHIAVFPNAQSDÄVFHALMKAGCIQLALNKICSKDSAFVP LLSCHTANIESTSILKALHYMYQTSTFRAEKLVENDFEALLWKTRCNLNHLMSQDDI KILKSLPCYKSISGRYGTCYVLTKSTPSAEVERWTQSSSSAFLEEKIHLKEL YEVIGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLSSAEELSEIKEQLFEK GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEENEIEVEGLPLLITLDSVLQTFDAKRPK FLTTYHELIPSRKDLFMNTLYLKYSNILLNCKVAKVFDISSFADLLSSVLPREYKTKS CTKWKDNFASESWLKNAWHFISESVSVKEDQEETKPTFDIVVDTLKDWALLPGTKFTV LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYNCIHEDMKRLLPVVRA PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY RLKHLLLEIGFNLVYNCDETANLYHCLIDADIPVSYVTPADIRSFLMTFSSPDTNCHI KVSEISSVPASDRMVQNLLDKLRSDGAELLMFLNHMEKISICEIDKSTGALNVLYSVK GKITDGDRLKRKQFHASVIDSVTKKRQLKDIPVQQITYTMDTEDSEGNLTTWLICNRS GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH SVDDGITLYQENITNACYKYLHEALMQNEITKMSIIDKLKPFSFILVENAYVDSEKVS FHLNFEAAPYLYQLPNKYKNNFRELFETVGVRQSCTVEDFALVLESIDQERGTKQITE ENFQLCRRIISEGIWSLIREKKQEFCEKNYGKILLPDTNLMLLPAKSLCYNDCPWIKV ACIIIKLENFMQQKV" 2256 c 2487 KYSFQRFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA DVLQLLWTSCPILPEKATPLSIKEQEGSDLGPQEQLEQVLNMLNVNLDPPLDKVINNC RNICNITILDEEMVKTRAKVLESIYEELSAEKREEFROLRGVAEVMVEDGWKLLKPEE VVINLEYESDEKPYLIKLPLELGTFHOLFKHLGTEDIISTKOYVEVLSSILFKNESEK LDPNEMRTVKRVVSGLFRSLQNDSVKVRSDLENVRDLALYLPSQDGRLVKSSILVFDD NQPFTEDDVRGIQNLGKGTKEGNPYKTGQYGIGFNSVYHITDCPSFISGNDILCIFDPHARYAPGATSISPGRMFRDLDADFRTQFSDVLDLYLGTHFKLDNCTMFRFPLRNAEMA KDTTVKYCHADIPREVAVKLGAVPKRHKALERYASNVCFTTLGTEFGQKEKLTSRIKS ILNAYPSEKEMLKELLQNADDAKATEICFVFDPRQHPVDRIFDDKWAPLQGPALCVYN ALAMTLKSATDNLISDTSYLIAMLGCNDIYRIGEKLDSLGVKYDSSEPSKLELPMPGT PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR LESLLIIHDANSRLKQAKHFYDRTVRVFEVMLPEKLFIPNDFFKKLEQLIKPKNHVTF MTSWVEFLRNIGLKYILSQQQLLQFAKEISVRANTENWSKETLQNTVDILLHHIFQER VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT LYTAEHQDIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKEVAK DFSVICQGFYEDIAHGKGKELTKVFSDGSTWVSMKNVRFLDDSILKRRDVGSAAFKIF KEIWKTDTKGRWNTTFMRHVIVKAYLQVLSVLRDLATSGELMDYTYYAVWPDPDLVHD QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT YLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSD SIPPLFSGRESHKTSSKHQSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRRL NSSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPEESSQSRDSAPSTPTSPTEFLTPGLR EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL MDLLSGNFLKELSLIPFLCPERAPAEFIRFHPQYQEVNGTLPLIKFNGAQVNPKFKQC  ${\tt RRLGLVPCGAVGVQLSEIQDQKWTVKPHIGEVFCYLPLRIKTGLPVHINGCFAVTSNH}$ 9

BASE COUNT ORIGIN 4163

20 밁 δ 밁 Q δÃ 밁 밁 Query Match Best Local : Matches 12261 12201 181 121 61 Н ATTTATATAGTGTGGATGAACAGGATGCAATCTTTTGTTGTCTAAAGGTGCTGCAGTTAA 12440 atttatatagtgtggttgaacaggatgcaatcttttgttgtctaaaggtgctgcagttaa Similarity 100.0%; Score 593; DB 9; 1 ilarity 100.0%; Pred. No. 1.3e-308; Conservative 0; Mismatches 0; Length 12793; Indels 0; Gaps 240 12320 0

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AL157766.9
                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Apr 12, 2001 this sequence version replaced gi:12709868. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either denial corresponding to the property of the sequence was finished as follows unless otherwise noted: all regions were either denial corresponding to the property of the sequence was finished as follows unless otherwise noted: all
IMPORTANT: This sequence is not the entire insert of clone RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-760Ml is at 92594 in this sequence.
                                                                                                                               RP11-40020 is from the library RPCI-11.1 of Pieter de Jong. For further details se
                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from 13q12.11-12.2, complete
                                                                                     VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                         //www.chori.org/bacpac/home.htm
                                                                                                                                                                       /www.sanger.ac.uk/HGP/Chr13
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="Alusq repeat:
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24769. .24891
                                         /note="AluY repeat: 47477. .47873
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39790. .40093
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27150. .27653
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2390. .2485
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                                                                                                                                                                                                                                                                                                                      restriction
                                                                                                                                                                                                                                                                                                                               /note="Single clone region. Assembly confirmed by
restriction digest data."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28522.
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19644. .19873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="q12.11-12.2"
                                                                                                       /note="AluY
                                                                                                                                                                                           /note="13 copies 4 mer tggt 88%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSx repeat: matches 1.
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/note="AluSg1 repeat: matches 1.
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                        5950. .6322 of consensus"
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                                   /note="AluJb repeat: 69748. .69930
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                      /note="MER31A repeat: matches 47. 71780. .72075
                                                                                                                                                                                                        /note="AluSx repeat: matches 1.
49168. .49212
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluY repeat: matches 1. .129 of consensus"
62330. .62363
                                                                                                     /note="MIR repeat: matches 6.
                                                                                                                                                                                                                                                                55068. .65395
/note="L1PB2_repeat: matches 5405.
                                                                                                                                                                                                                                                                                             /note="TIGGER1 repeat: matches
                                                                                                                                                                                                                                                                                                                     /note="AluY repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                            /note="TIGGER1 repeat: matches 46.
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                                                                                                                                                                                                                                                                                                                                                                                           /note="TIGGER1 repeat:
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57357. .57392
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53978. .54137
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). .58389
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2 (bases 1 to 99819)
Waterston, K.H.
Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
                                                          The sequence of Homo sapiens Unpublished
                                                                                                                                                                                                              PROGRESS ***,
AC079761
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                                                                                                                           Mammalia;
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Eutheria; Primates;
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Pred. No. 1.3e-308;
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be preserved.
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21395. .22944
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27331. .28778
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24522. .25870
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1238. .2538
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25971. .27230
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                                                                                                                                                                                                                                                                                                                                                          /chromosome="UNK"
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52910 .55127
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64286. .67105
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30994. .32460
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SHGC-53325 Human Homo s
G36555
G36555.1 GI:2734222
STS.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
1 (bases 1 to 418)
                                                                                                                                                                Prepared
                                                                                                                                                                                                                             Buffer:
                                                                                                                                                                                                                                                                                                    Protocol:
                                                                                                                                                                                                                                                                                                                                                                                              Email: myers@shgc.stanford.edu
Primer A: GTGGAGGTGCAAACATTCCT
Primer B: ACATTTAATTCATGTTTGTCCCG
STS size: 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers,R.M.
Human STSs (1997)
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                                                                                /clone_lib="Human"
89. .290
89. .108
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65 c 55
                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="13"
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Primates;
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                                                                                                           Lab
                                                                                                                                                                                                                                                                                                                       Submitted (09-MAR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fis (full insert sequence); oligo capping.
Macaca fascicularis adult male frontal lobe left cDNA to mRNA,
clone_lib:macaque brain cDNA library QflA clone:QflA-15307.
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Macaca fascicularis brain cDN
sequence.
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Hashimoto, K., Osada,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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/tissue_type="frontal lobe
/clone_lib="macaque brain c
                              /sex="male"
                                           /db_xref="taxon:9541"
/clone="QflA-15307"
                                                                                                 Location/Qualifiers
                                                                       /organism="Macaca fascicularis'
                                                                                                                                                                                                                                                                   pME18S-FL3 (ACC.NO.
DraIII (CACTGTGTG)
DraIII (CACCATGTG)
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Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleoti methods of use thereof
Patent: W0 0140521-A 3903 07-JUN-2001; Curagen Corporation (US)
Location/Qualifiers
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Sequence
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                                                                                                /note="1 of 2 allelic variants
Accession number cg43924289"
8 c 8 g 20 t
                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
26
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CIIIKLENFIQOKV"
a 552 c 653 g 1022 t
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LAMTLKSATDNLISDTSYLIAMLGCNDIYRIGEKLDSIGVKYDSSEPSKLELPMPGTP
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SSFLGKIYQIDIGYSEYKIVSSLDLYKFSPDDESSQSRDSAPSTPTSPTEFLAPGLRS
IPPLESGRESHKTSSKHOSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRLY
LKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/note="Host: TOP10; Vector: pME18S-FL3 (Acc.No.
R. Site1: DraIII (CACTGTGTG); R. Site2: DraIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSFQRFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEARR
WLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALVAADYAVRGKSDKDVKPTALAQ
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                     Score 51;
Pred. No.
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Pred. No. 1.8e-40;
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DB 6; Lc.
3.5e-16;
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1 (bases 1 to 50)

Shimkets,R.A. and Leach,M.

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof patent: WO 0140521-A 3906 07-JUN-2001;

Curagen Corporation (US)
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1 (bases 1 to 51)

Shimkets,R.A. and Leach,M.

Nucleic acids containing single nucleotide polymorphisms and mathematical containing single nucleotide polymorphisms.
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Sequence 3905 from Patent
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Sequence 3906 from Patent
AX160578
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Patent: WO 0140521-A 3905 07-JUN-2001;
Curagen Corporation (US)
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Accession number cg43924289"
8 c 8 g 15 t
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                        /note="2 of
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J. 3.5e 0;
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1 (bases 1 to 50)
Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide methods of use thereof
Patent: WO 0140521-A 3902 07-JUN-2001;
Curagen Corporation/Qualifiers
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AX160576
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AX160574
AX160574.1 GI:14541905
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Patent: WO 0140521-A 3904 07-JUN-2001;
Curagen Corporation (US)
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
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Accession number cg43924289"
8 c 9 g 20 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 51)
Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0140521-A 3901 07-JUN-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:18307375.
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                              Center code: SC
                                       Center: Wellcome Trust Sanger Institute
                                                                                                                            Direct Submission
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                           HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                         AL670276.2 GI:18477095
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/db_xref="taxon:9606"
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Consensus quality: 146474 bases at least Q40
Consensus quality: 146902 bases at least Q20
Consensus quality: 147368 bases at least Q20
Insert size: 148128; sum-of-contigs
Insert size: 154153; 3.3% error; agarose-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Center project name: bM15D21

Summary Statistics
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                                                                                         Similarity
                                                                        3.9%; Score 23; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                             /note="assembly_fragment:00876
fragment_chain:1"
139660. .149128
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/note="assembly_fragment:01606
fragment_chain:1"
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fragment_chain:1"
9321. .12084
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33291 c 33024 g
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fragment_chain:1"
22474..30439
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fragment_chain:1"
133141. .139559
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17877...22373
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fragment_chain:1"
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1. .4701
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VERSION
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AUTHORS
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JOURNAL
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On Feb 5, 2002 this sequence version replaced gi:18201826.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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Submitted (20-JUN-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 336028)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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137883
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g of 3231 bp in length
of unknown length
g of 2662 bp in length
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g of 29709 bp in l
f unknown length
g of 45451 bp in l
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g of 39295 bp in
f unknown length
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f unknown length
g of 9539 bp in 1
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of 7321
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of 10736 bp in length
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of 7741
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of 6613
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of 4877
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of 6549
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Search completed: May 22, Job time: 11900 sec
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1. .336028
            2002, 08:50:10
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Perfect score:
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                                                                                                                                                             Pred. No.
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seq length: 2000000000
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1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
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Result No.	Score	Query Match	Query Match Length DB	DВ	ID	Description
μ.	593	100.0	1317	22	AAS29058	cDNA encoding for
2	593	100.0	12792	22	AAH20176	Human mutated spas
ω	593	100.0	12793	22	AAH20174	Human spastin nucl
4.	593	100.0	12793	22	AAH20178	Human mutated spas
υī	593	100.0	12793	22	AAH20179	Human mutated spas
6	593	100.0	12793	22	AAH20182	Human mutated spas
7	430	72.5	1387	22	AAS29132	cDNA encoding for
80	51	8.6	51	22	AAI76962	Human silent SNP c
9	51	8.6	51	22	AAI76964	Human silent SNP c

31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0190076.

17-JAN-2001; 2001WO-US01305

02-AUG-2001 WO200155162-A1 Homo sapiens.

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	œ	Human cDNA sequenc	Human ORFX ORF2695	Human nervous syst	Human secreted pro	Genomic sequence #	Genomic sequence #	Ø	a h	one	Probe #1604 used t	usec	Probe #1620 for ge		Human brain expres		foetal	Human breast cell	Human secreted pro	Human gene regulat		immune	immune	a			Drosophila melanog		CDNA	EST clone DM420.	æ	silent SNP	Human silent SNP c		Human silent SNP c

## ALIGNMENTS

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2000US-0198123. 2000US-0205515. 2000US-0209467.

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The present invention relates to the isolation of novel DNA-binding proteins (AAU18154-AAU18281), and cDNA and genomic sequences encoding
                                               Claim
                                                                          Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers -
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P-PSDB; AAU18182.
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CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO
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Query Match Best Local Similarity

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593; DB 22; No. 1.7e-272;

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(ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome
                                                                                                                                                                                   markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (1). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin that the protein of the prot
                                                                               N.B. The present sequence is derived from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYMC-)
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                                                                                                                                 protein or spastin gene expression or encodes a mutated human spastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to Cc (Arsacs)) gene sequences (I). The spastin gene has been mapped to Cc chromosome 13q11 (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists (I), their fragments Cc or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the Cc diagnosis of an early onset neurodegenerative disease in an individual. Cc The neurodegenerative disease comprises reduced sensory nerve conduction, creduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and Cc annormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome cc markers, to identify genetic disorders, as hybridisation probes or Cc analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin
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                                       encodes human spastin as given in
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                                       gene expression or activity. The present tin as given in the present invention.
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The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC acid molecule in a sample (I) is useful for diagnosing or aiding in the CC acid molecule in a sample. (I) is useful for disease in an individual. (CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or cromosome contents.
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                                                                                                                                                                                                                                                                          Claim
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N.B. The present sequence is not given in the present specification but is derived from the human spastin nucleotide sequence (AAH20174) as
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nerative disease; reduced sensory nerve conduction; diagnos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rne present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective antiquition and the sequences of the sequenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein or spastin gene expression or activity. The present sequence encodes a mutated human spastin.

N.B. The present sequence is not given in the present specification to derived from the human spastin nucleotide sequence (AAH20174) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12793
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                                                                                                                                                                                                                                                                              Homo sapiens.
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New isolated polynucleotide, encoding spastin gene, and polypeptides

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The present invention describes human and mouse spastin, and mutated C(human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay C(ARSACS)) gene sequences (I). The spastin gene has been mapped to Cc chromosome 13q11. (I) have neuroprotective activities and can be used in Gene therapy and as a spastin polypeptide agonists. (I), their fragments C acid molecule in a sample. (I) is useful for diagnosing or aiding in the C diagnosis of an early onset neurodegenerative disease in an individual. C The neurodegenerative disease comprises reduced sensory nerve conduction, creduced motor nerve velocity, hypermyelination of retinal nerve fibres, c atrophy of upper cerebellar vermis, absence of Purkinje cells and C abnormal neuronal lipid storage. (I) can also be used to produce markers, to identify genetic disorders, as hybridisation probes or C analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from C analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from C the present invention can be used to identify subjects having or at risk of developing a disorder associated with aberrant expression C analysis, of (I). The assays can be utilized to identify a subject C having or at risk of developing a disorder associated with Spastin C encodes a mutated human spastin or activity. The present sequence C encodes a mutated human spastin nucleotide sequence (AAH20174) as C stated on page 14.
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02-MAR-2000;
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18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromatin organisation modifier; y-box binding property of the control of the chromatic disease; genetic autoimmune disorder; rheumatic disease; genetic infectious disease; neurological disorder; gene
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26-JUL-2000;
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11-JUL-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulatory; anti-HIV;
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2000US-02266279

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2000US-02271868

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2000US-0229344
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nalignant disease;
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2000US-0231414 2000US-0232080 2000US-0232081 2000US-0231968 2000US-023196 2000US-0232398 2000US-0232398

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CC proteins (AAU18154-AAU18281), and cDNA and genomic sequences encoding CC proteins (AAU18154-AAU18281), and cDNA and genomic sequences encoding CC for these proteins. DNA-binding proteins such as histones, chromo CC (chromatin organisation modifier) domain proteins, and Y-box binding CC proteins may contribute to diseases resulting from aberrant DNA CC organisation and/or gene transcription. The sequences of the invention CC are useful in screening assays to identify antagonists and/or agonists CC that may enhance or block activities mediated by DNA-binding proteins. CC such as malignant diseases (e.g. cancer), autoimmune disorders CC (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatold CC arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious CC diseases (e.g. HIV) and neurological disorders (e.g. Alzhelmer's CC diseases (e.g. The polynucleotide sequences of the invention may also be CC used in gene therapy. AAS29030-AAS29157 represent cDNA sequences CC encoding for novel DNA-binding proteins.

CC Note: The sequence data for this patent did not form part of the printed Specification, but was obtained in electronic format directly from WIPO CX at ftp.wipo.int/pub/published_pct_sequences.
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08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecules encoding human secreted chromosomal binding proteins; used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-465557/50.
P-PSDB; AAU18256.
                                                                                                                                                                                                                                                                                                                            Sequence
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AAIT3060 to AAIT9867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs). AAM53114 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999; 99US-0168138
29-NOV-2000; 2000US-0726173
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      AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide CC sequences (I), which contain single nucleotide polymorphisms (SNPs). AAM53114 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. CC ror example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of complements own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The production of antibodies specific for polymorphic polypeptides. The
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29-NOV-2000; 2000US-0726173.
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         C polynoclectide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polynorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the polypeptides by expressing inactive proteins or to supplement the complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The conditions of antibodies should be used as diagnostic agents for detecting the antibodies may also be used as diagnostic agents for detecting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acid sequences, useful in
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29-NOV-2000; 2000US-0726173.
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Sequence
                                                                                                                                                                                                                                                              AAM53114 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and proto
                                                                                                                                                                                                                                                                                                           AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1246;
                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acid sequences, useful in genetic testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2000; 2000WO-US32758
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51
BP;
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14
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                                                                                                                                                                                                                                                                                           contain single nucleotide polymorphisms (SNPs)
8 C;
9
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G;
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Pred. No.
20
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T; 0 other;
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2.4e-06;
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RESULT I ANT 6961 ID ANT 6961 ANT 6961 ANT 6971 ANT XXX Hum XXX Hum XXX Hum XXX Hom XXX Hom XXX Hom XXX Hom XXX Hom XXX ANT 697 ANT 607 ANT 60
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                                                 QΥ
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CC AAM53114 to AAM5329 represent peptides related to human polymorphic CC polynucleotide sequences. The sequences can be used in gene and protein CC therapy, and in vaccine production. (I) and the polypeptides encoded by C them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate expression of polymorphic polypeptides. CC For example, (I) may be used to treat disorders by rectifying mutations CC or deletions in a patient's genome that affect the activity of CC polypeptides by expressing inactive proteins or to supplement the CC patients own production of polypeptide. Additionally, (I) and its CC complementary sequences may also be used as DNA probes in diagnostic cassays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be used as antigens in the CC production of antibodies seconded by (I) may be used as antigens in the CC antibodies may also be used to down regulate expression and activity. CT he antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides.
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                                                                                                                                                                                                                                                     Sequence
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29-NOV-2000;
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acatcttatgtttacaggcttcct 50
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                                                                                                               Similarity 100.
24; Conservative
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2000US-0726173.
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C;
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Pred. No.
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0.14;
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                                                                                                                 Indels
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28

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RESULT 14 AAS45491/c

AAS45491;

AAS45491 standard; DNA; 4604

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RESULT 13
AAI76960
ID AAI769
                                                                                          CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide CC sequences (I), which contain single nucleotide polymorphisms (SNPs). CC AAM53114 to AAM53329 represent peptides related to human polymorphic CC polynucleotide sequences. The sequences can be used in gene and protein CC therapy, and in vaccine production. (I) and the polypeptides encoded by CC them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate expression of polymorphic polypeptides. CC for example, (I) may be used to treat disorders by rectifying mutations CC or deletions in a patient's genome that affect the activity of CC polypeptides by expressing inactive proteins or to supplement the polypeptides by expressing inactive proteins or to supplement the CC complementary sequences may also be used as DNA probes in diagnostic CC cassays to detect and quantitate the presence of similar nucleic acids CC in samples, and therefore which patients may be in need of restorative CC therapy. The polypeptides encoded by (I) may be used as antigens in the CC production of antibodies seconded by (I) may be used as antigens in the CC antibodies may also be used to down regulate expression and activity. CT he antibodies may also be used as diagnostic agents for detecting the
 Matches
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic nucleic acid sequences, useful in genetic testing therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-356160/37
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                                                                                        Sequence 51 BP; 12 A; 8 C; 3 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1245; 2653pp; English
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                                                                                                                         of polymorphic
 Conservative
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                    100.0%;
                                                                                                                         polypeptides in samples
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 0;
                  Score 24;
Pred. No.
 Mismatches
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                  DB 22;
. 0.14;
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 0
                                 Length 51;
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EST clone DM420

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RESULT 1
AAV90383
ID AAV9
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AC AAV9
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DT 15-E
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Best Local S
Matches 21
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Designing primers and probes for analysing diseases associated cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified gassociated with cell cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                              AAV90383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                    AAV90383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4604 BP;
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                                                                                                                                                                                                                                                          immunosuppressive; antitumour; cytostatic;
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                                                                                                                    standard; cDNA; 268
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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  (first entry)
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Pred. No.
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Search completed: May Job time: 6652 sec

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Query Match
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Matches 20
                                                                                                                                                                                                                                               The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haematopolesis regulating chemotactic/chemokinetic activity, activin/inhibin activity, chemotactic/chemokinetic activity, activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 523; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding human secreted proteins - de
e.g. human blood, kidney, foetal lung, placenta, testes,
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                                                                                                                                                                                                             Sequence
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pituitary, retina and colon cDNA libraries.
                                                                                             Similarity 20; Conserv
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1: /cgn2_6/ptodata/1,

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US-08-06-775C-1
US-09-054-775C-1
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US-09-305-639-4
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US-09-490-558-96
US-09-284-782-34
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US-09-284-782-35
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Sequence 219, App	Sequence 219, App	Sequence 219, App	Sequence 68, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 21, Appl	Sequence 1, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 31, Appl	•		Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 24, Appl

## ALIGNMENTS

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; TISSUE TYPE: ; CELL TYPE: 1
US-08-843-417-1
                                                                                                                                                                                TELEFAX: (415) 324-0638
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHER
TITLE OF INVENTION: TETRODOTOXIN-RE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/843
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 2834
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
                                                             MOLECULE TYPE: cDN
MYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 525 Univ
CITY: Palo Alto
STATE: CA
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TETRODOTOXIN-RESISTANT
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08450065 Patent No. 5798105 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 56
LENGTH: 164
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cunnigham, Mary Jane
APPLICANT: Zweiger, Gary B.
APPLICANT: Panzer, Scott R.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: MONITORING TOXICOLOGICAL RESPONSES
FILE REFERENCE: PA-0011 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 700625315H1
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schoenmakers, Johannes
APPLICANT: Konings, Rudolph NH
APPLICANT: Moelans, Inge IMD
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APPLICANT: Moelans, Inge IMD
TITLE OF INVENTION: NO. 579810
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CITY: King of Prussia
FILING DATE
                                                                APPLICATION NUMBER: US/0. FILING DATE: 25-MAY-1995
                  APPLICATION NUMBER:
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                             19406-0939
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Pred. No.
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-270-5090 INFORMATION FOR SEQ ID NO:
                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                         REFERENCE/DOCKET NUMBER: B2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5065
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: 16K
              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: | ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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stre: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                              TELEPHONE: Z15 TO TO NO:
                                                                                                                                                                                                                                                                                                                                                                              STREET: UW2220, PO BOX
CITY: King of Prussia
                                                                                                         NAME: Jervis, Herber
REGISTRATION NUMBER:
                                                                                                                                                                                                              FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: PLASMODIUM STRAIN: FALCIPARUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moelans,
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                                                                                                                                                                                                                                                                                                         Floppy disk
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
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APPLICANT: Takash
                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2659 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REGISTRATION NUMBER: 3,367
REFERENCE/DOCKET NUMBER: 'TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                        TOPOLOGY: 1:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Takashi UENO et al. TITLE OF INVENTION: MboI RESTF
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                                                                                                                                                                                                        ANTI-SENSE:
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10900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 199301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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                                   STRAIN: 10900 INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                       H: 2659 base pairs
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805 Fifteenth Street, N.W., #700
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                                                                                                                                                                                                                                                                                                           linear
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IBM Compatible
SYSTEM: MS-DOS
                                                                                               Moraxella
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Pred. No.
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. 49;
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APPLICANT: MASUDA, T
APPLICANT: SUZUKI, Y
APPLICANT: YABUTA, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Applic Patent No. 5885821
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,918
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8:
FILING DATE: 04-MAR-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1208 TAAAAACATCAAAAATT 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: OTHER INFORMATION: /n PUBLICATION INFORMATION: AUTHORS:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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LOCATION:
                                                                                                                                                                                                                            STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                STATE: Virginia COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08805918
                                                                                                                                                                                                                                                      EE: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                 YABUTA, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.9%;
                                                                                                                                                                                                                                                                                                                   PROCESS FOR PRODUCTION OF SECRETORY KEX2 DERIVATIVES
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                                JP 8-073217
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Pred. No.
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FILING DATE: 16-DEC-1996 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

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, Donna M.
, Donna M.
, 36,607

001560-295

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; LOCATION:
US-08-805-918-1
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                                                                                        CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31 MAR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08464402
Patent No. 5858705
GENERAL INFORMATION:
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3417 BASE PAIRS
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 1:
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MOLECULE TYPE: C
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                            SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/464,402
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2848 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00: TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WEI, ET TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Saccharomyces cerevisiae STRAIN: X2180-IB
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS:
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                                                                                 201-994-1744
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/ 100.0%; Pr
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Pred. No.
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RESULT

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SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-054-775C-1
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                                                            Matches
                                                                         Best Local
                                                                                       Query Match
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                                                                                                                                                                                                                                                       TELEFAX: 301-309-8439 INFORMATION FOR SEQ ID NO: 1:
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                  232 tgcagttaaaaaaaaaa 248
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/464,402
FILING DATE: 05-UN-1995
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31-MAR-1995
ATTORNEY,AGENT INFORMATION:
NAME: HOOVET, KENLEY K.
REGISTRATION NUMBER: 40,302
REFERENCE,DOCKET NUMBER: PF161D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3417 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/054,775C
FILING DATE: 03-Apr-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human DNA Ligase III
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                                                         l Similarity
17; Conserv
                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                       TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                            Conservative
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Pred. No.
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Pred. No.
                                                            Mismatches
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46;
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                                                            Indels
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                                                           Gaps
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US-08-702-572-14/c

Sequence 14, Application US/08702572 Patent No. 5965386

GENERAL INFORMATION:

APPLICANT: Kerry-Williams, Sean M
APPLICANT: Gilbert, Sarah C
TITLE OF INVENTION: Yeast Strains and Modified Albumins

NUMBER OF SEQUENCES:

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RESULT 10
5521093-4/c;
Patent No. 5521093
                                                                                                                                                                                                                                                                                                                    ş
                                                                                                                        APPLICANT: LEMOINE, YVES;NGUYEN, MARTINE;ACHSTETTER, TILMAN TITLE OF INVENTION: YEAST VECTOR CODING FOR HETEROLOGOUS;GENE FUSIONS LINKED VIA KEX2 CLEAVAGE SITE AND CODING FOR TRUNCATED KEX2 GENES
                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9
Best Local Similarity 100.
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO 95/23857
FILING DATE: 1-MAR-1995
APPLICATION NUMBER: GB 9404270.2
FILING DATE: 5-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Naomi Biswas
REGISTRATION NUMBER: 38,384
REGISTRATION NUMBER: 38,384
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 191,354
FILING DATE: 07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610/878/4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09
FILING DATE: 11-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: MicroSoft Word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                       NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
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CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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1020 First Avenue
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100.0%; Pr
100.0%; O;
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                                                                       US/08/393,025
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0; Mismatches
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; TYPE: DNA; Homo sapiens US-09-305-639-4
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; TYPE: DNA; Homo sapiens US-09-305-639-1
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Best Local Similarity
Matches 17; Conserv
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                                                                           SOFTWARE: FastSEQ
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09305639 Patent No. 6200778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/016001
CURRENT APPLICATION NUMBER: US/09/305,639
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,663
EARLIER FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09305639 Patent No. 6200778
                                                                                                                                                                    APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
APPLICANT: Selden, Richard F
TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
FILE REFERENCE: 07236/016001
CURRENT APPLICATION NUMBER: US/09/305,639
CURRENT FILING DATE: 1999-05-05
                                                                                                                EARLIER APPLICATION NUMBER: 60/084,663
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                           LENGTH:
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FILING DATE: 04-MAR-1993
APPLICATION NUMBER: 500,885
FILING DATE: 29-MAR-1990
                                                         7622
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100.0%; Pred. No.
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                                                                      Sequence 200, Application US/08835728D Patent No. 6017704
GENERAL INFORMATION:
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Best Local Similarity

Matches 16; Conserv
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GENERAL INFORMATION:
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FILING DATE: June 03, 1996,
ATTORREY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                           APPLICANT: Herman, APPLICANT: Baylin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 422.
CITY: La Jolla
CMATE: CA
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APPLICANT: Baylin,
TITLE OF INVENTION:
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                            APPLICANT: Baylin, TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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FILING DATE: April 11, 1997
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EDNESS: single
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                          Methylation Specific Detection
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Pred. No.
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Matches 16; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Herman, Jame APPLICANT: Baylin, Step TITLE OF INVENTION: Met NUMBER OF SEQUENCES: 21 CORRESS:
                                                                                                                                                                              ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 29 base pairs
TYPE: nucleic acid
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MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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APPLICATION NUMBER: 0
FILING DATE: June 03,
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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STREET: --
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FILING DATE: April 11, 1997
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OPERATING SYSTEM:
SOFTWARE: PatentI
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Methylation Specific Detection
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ER: 07265/125001
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566	530	460	428	302	292	230	201	677	478	162	818	712	236	727	1079	203	840	789	1016	418	287	483	349	441	351	739
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BM119091	BM118416	AI506773	BE862199 .	AI865982	AI447763	BB297230	AV167991	BF576822	BI871763	BE894617	BI599024	AV716805	AA228008	BG619034	BM476997	AA228047	BF693898	BE889418	BE896315	N46342	T17045	N48291	AI561086	N59442	AW262498	AL567149
BM119091 L0920E06-		AI506773 vm58g10.x		AI865982 wk88g03.x	AI447763 mg82f11.x		AV167991 AV167991	BF576822 602132834			4	AV716805 AV716805			7	AA228047 zr58a07.r	8	BE889418 601512535	BE896315 601439161	N46342 yy74a10.s1			S.		AW262498 xq85c06.x	AL567149 AL567149

## ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 AI803488/c LOCUS SOURCE ORGANISM ACCESSION VERSION FEATURES COMMENT KEYWORDS DEFINITION JOURNAL source Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index EST AI803488 500 bp mRNA linear tc17902.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone 3', mRNA sequence.
AI803488 500 bp mRNA linear l Unpublished (1997) AI803488.1 GI:5368882 Mammalia; Eutheria; 1 (bases 1 to 500) pregnant uterus //lab\_host="pH10B" //lab\_host="pH10 /clone="IMAGE:2064146" /clone\_lib="Soares\_NhHMPu\_S1" /tissue\_type="Pooled human melanocyte, fetal heart, pregnant uterus" /organism="Homo sapiens" /db\_xref="taxon:9606" ocation/Qualifiers Hominidae; Euteleostomí; EST 13-DEC-1999 IMAGE: 2064146 circles and

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JOURNAL COMMENT
                                                                                                                                                                                 REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
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                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 982 Std Error: 0.00
                                                                                                                                                                                                                                                                       A1932370 543 bp
wd27e11.x1 Soares_NFL_T_GBC_S1 F
IMAGE:2329388 3', mRNA sequence.
A1932370 GI:5671107
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 543)
                                                                                                                                                                                                                                   Homo sapiens
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National Cancer Institute, Cancer Genome Anatomy
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23; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                    Location/Qualifiers
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Local Similarity 100.0%;
nes 419; Conservative
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AGENCOURT_6463084 NIH_MGC_71
5', mRNA sequence.
EM470780
                            Unpublished (1999)
Contact: Robert Strausberg, Ph.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 828)
NIH-MGC http://mgc.nci.nih.gov/.
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Library Preparation: Life Technologies, Inc. Library Arrayed by: The I.M.A.G.E. Consortiu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by E Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2329388"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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mRNA sequence.
BE890125
BE890125.1 GI:
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                              BE890125
601513104F1 NIH_MGC_71
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb. "
a 107 c 138 g 321 t
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/db_xref="taxon:9606"
/clone="IMAGE:5533575"
/clone_lib="NIH_MGC_71"
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 GI:10348134
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                                           taacatatttcttttgcagaatgtaaaaggtaatgataattagtttatataagtgtactg
                                                                                                atttatatagtgtggttgaacaggatgcaatcttttgttgtctaaaggtgctgcagtt-a
                                                                                                                                                                                                                                                                                                                                   TATTAACTGTTAGAACACTTGCTTTATGTTTGTGTGTACATATTTTCCACAAATGTTATA
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                                                                                                                                                                                                                   AAAAAAAAACAACCTTTTCTTTCAATATGGCATGTAGTGGAGTTTTTTTAACTTTAAAAAA
                                                                                                                                                                                                                                                                          ATTTATATAGTGTGGTTGAACAGGATGCAATCTTTTGTTGTCTAAAGGTGCTGCAGTTAA
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 660)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph
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52; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
a 95 c 107 g 262 t
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..5e-137;
hes 1;
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TTTTTTACTTTTAT 594
            ttatatttccccatgaatgatcagaactgacatttaattcatgtttgtctcgccatgctt 411
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TTATATTTCCCCCATGAATGATCAGAACTGACATTTAATTCATGTTTTGTCTCGCCATGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2581479"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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35 gatagcaacggaaaactcaaaatggtggcagttcttattaccagttgttagtattgtttc

Matches

368;

Conservative

0;

62.1%;

Score 368; DB 9; Pred. No. 5.3e-1; Mismatches

5.3e-132;

Length 368

Indels

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Gaps

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RESULT 6
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Unpublished (1997)
Contract: will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL;
'info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 368)
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IMAGE:970551 3', mRNA sequence
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                  140
           /tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="sOLR (kanamycin resistant)"
/lab_host="sOLR (kanamycin resistant)"
/note="vector: Bluescript SK-; Site_1: EcoRI; Library
/constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide-
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
40 a 61 c 52 g 115 t
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/db_xref="taxon:9606"
/clone="IMAGE:970551"
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This clone is available royalty-free through LLNL;
IMAGE Consortlum (info@image.linl.gov) for further i
Seq primer: -40UP from Gibco
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7f68a06.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo
IMAGE:3299794 3', mRNA sequence.
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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BE856736.1 GI:10370063
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Location/Qualifiers
/note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSP pool 1: 103324-310919, 333208-325895 Soares NbHSP pool 1: 15002-150407, 151176-152327 Soares NbHSP-9W pool 1: 150407, 151176-152327 Soares NbHSP-9W pool 1: 150407, 151176-152327 Soares NbHSP-9W pool 1: 1758280-760583, 772104-774407 Soares NbHSP pool 1: 733720-726407, 739108-32663 Soares NbHOT pool 1: 723720726407, 739108-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
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1 to 536)
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Primates;
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                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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BF438152.1
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7q67f12.x1 NCI_CGAP_Lu24 Homo
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National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 536)
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                                                                                                                                                                                                                                                                                  Emmert-Buck, M.D., Ph.D
                                                                                                                                                                                                                                                                                                Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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                                                                                                                                                              High quality sequence stop: 481.
                                                                                                                                                                                                     Enmert-Buck, M.D., rn.u.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                            info@image.llnl.gov
Seq primer: -40UP from Gibco
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/organism="Homo sapiens"
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/clone="inb="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="hH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were
                                                                                                                                             Location/Qualifiers
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IMAGE:3703462 3',
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                                                                                                                                                                        High quality sequence stop: 456.
Location/Qualifiers
                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1085 Std Error: 0.00
                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy
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AI217518.1 GI:3797333
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soares and M. Fatima Bonaldo.

85 c 67 g 172 t
       /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="PH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized
                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:1845278"
                                                                                                                                     /organism="Homo sapiens"
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Pred. No.
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o sapiens
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s cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATCAGAACTGACATTTAATTCATGTTTGTCTCGCCATGCTTCTTTACTTTAACATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTTAAAATCATTGTGTTATCTAGTAGTTATAATTATCGGCTTATATTTCCCCCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AIO78834 422 bp mRNA linear cz46d05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone 3', mRNA sequence.
AIO78834 AIO78834.1 GI:3413141 EST.
                                                                                                                                                 This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 361.
                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                     Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 422)
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1678377"
/tissue_type="Pooled
pregnant uterus"
                                 /clone_lib="Soares_NhHMPu_S1"
                                                                                                                                   Location/Qualifiers
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100.0%;
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Pred. No. 3.5e-123;
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                   human melanocyte,
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                   fetal
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IMAGE:1678377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341;
                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Me
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA954825
oo99d10.sl NCI_CGAP_Kid6
CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consorthum/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 2008 Std Error: 0.00
                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 410)
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National Cancer Institute, Cancer Genome Ana
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                                                                                                                             Emmert-Buck, M.D., Ph.D.
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Pred. No.
                                                                                                                                               Jeffrey Medeiros, M.D.,
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                                                     Sequencing Center information can b
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IMAGE:1574323 3',
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                                            white, Y., Wylie, T., WashU-NCI human EST I Unpublished (1997)
Contact: Wilson RK
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1 (bases 1 to 528)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
Krizman,D., Kucaba,T., Lacy,M., Le,No, Lennon,G., Marra,
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Thei
White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                              AA417817 528 bp zv04h08.rl Soares_NhHMPu_S1 Homo similar to gb:J03464 PROCOLLAGEN
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800
                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                );, mRNA sequence.
AA417817
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="kidney tumor"
/lab_host="SOUR (kanamycin resistant)"
/note="organ: kidney; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCACGAG; 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb.
a 64 c 51 g 133 t
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/db_xref="taxon:9606"
/clone="IMAGE:1574323"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Kid6"
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100.0%; Pred. No. 2.3e-117;
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                                                                                                                                                                                                                                                                                                                 sapiens cDNA clone IMAGE:752703 5 ALPHA 2(I) CHAIN PRECURSOR (HUMAN
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SOURCE
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                                                                   EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infolmage.llnl.gov) for further information. Insert Length: 812 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 455.
                                                                                 AI499896.1
                                                                                                mRNA sequence.
AI499896
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                                                                                                                                                                                                                                                 511
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/clone="IMAGE:752703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:5975541"
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/tissue_type="Pooled human me:
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                                                                                 GI:4391878
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Pred. No.
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                                                                                                                            sapiens cDNA clone
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                                                                                                                                                                                                                                             364 atgaatgatcagaactgacatttaattcatgtttgtctcgccatgcttctttactttaac
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Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 404)
                                                Homo sapiens
                                                                                                                              mRNA sequence.
                                                                                                                                            nw66c04.s1 NCI_CGAP_GCB1
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DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution if found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1662 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                  human
                                                                                 EST
                                                                                                AA809783.1 GI:2879189
                                                                                                                AA809783
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High quality sequence stop: 395.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

1 64 c 52 g 139 t
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/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%;
                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.4e-102;
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                                                               164
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                                                                                                                                                                                                                                                     404 CATGTAGTGGAGTTTTTTTAACTTTAAAAACATCAAAAATTGTTAAAATCATTGTGTTAT 345
104
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             ttgcacctccacattttattgctt 593
                                                           AATTAAGGGCTTACAGAACATGTTGAAACTTTTTTTACTTTTATTGGGAATAAGGAATGT
                                                                              aattaagggcttacagaacatgttgaaactttttttttacttttattgggaataaggaatgt 569
                                                                                                                       taatgataattagtttatataagtgtactggctgtaaatgatgctaaatatactttatgc 509
                                                                                                                                                                                                       tcatgtttgtctcgccatgcttctttactttaacatatttctttttgcagaatgtaaaagg 449
TTGCACCTCCACATTTTATTGCTT 81
                                                                                                                                                                                      TCATGTTTGTCNCGCCATGCTTCTTTACTTTAACATATTTCTTTTGCAGAATGTAAAAGG
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Insert Length: 643 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 397.
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CDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:9606"
/clone="IMAGE:1251558"
/clone_lib="NCI_CGAP_GCB1"
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Matches 240; Conserv
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                                                                                                                                                                                                                                                                catttaattcatgtttgtctcgccatgcttctttacttttaacatatttcttttgcagaat 441
                                                                     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 836 Std Error: 0.00 Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Wilson RK
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Location/Qualifiers
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//lab host-"DHIOB"
//lab host-"DHIOB"
//note-"Organ: mixed (see below); Vector: pT7T3D-Pac
//note-"Organ: mixed (see below); Vector: Site_1: Not I;

Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 448488-489479."
31 a 101 c 81 g 143 t
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/db_xref="GDB:5975490"
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## ALIGNMENTS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12793)

1 (bases 1 to 12793)

1 Hudson, T. J., Engert, J. and Richter, A.

Identification of arsacs mutations and methods of use therefor Patent: WO 0129266-A 1 26-APR-2001;

PACGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)

Location/Qualifiers
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Sequence 1 from Patent W00129286.
AX119931 GI:14036678
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                  4163 a
              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                       Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital, 1650 Cedar Ave., Montreal, QC H3G 1A4, Canada Location/Qualifiers
                                                                                                                                                 Engert, J.C., Berube, P., Mercier, J., Dore, C., Lepage, P., Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J. and R.S., Morgan, K., Hudson, T.J. and Quebec, a spastic ataxia common in northeastern Quebec, by mutations in a new gene encoding an 11.5-kb ORF Nat. Genet. 24 (2), 120-125 (2000)
                                                                                                                                                                                                                     Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eucheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 12793)
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                                                                                            Direct Submission
                                                                                                                 Engert, J.C.,
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/map="between D13S232 and D13S292"
                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                GI:6907041
                                                                                                                  Berube, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 500; DB 6; 100.0%; Pred. No. 1.5e-256;
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                                                                                                                                                                                                                                                                                                                                12793 bp
                                                                                                                 Dore,C.,
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                                                                                                                 Lepage, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                 Ge,B.,
                                                                                                                   Hudson, T.J.
                                                                                                                                                                                                                                      Euteleostomi;
Homo.
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                                                                                                                                                                                                              Ge, B.,
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AL157766/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500;
requests: clonerequest@sanger.ac.uk
on Apr 12, 2001 this sequence version replaced gi:12709868.
During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                              Human DNA sequence from clone RP1
13q12.11-12.2, complete sequence
                                                                                                                                                                                                                                                               HTG
                                                                                            Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                 AL157766
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                                                                                                                                   Direct Submission
                                                                                                                                                      Tromans,
                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                AL157766.9
                                                                                                                                                                   (bases 1 to 92693)
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YLWHHDIKNPENHDIAWEVFKHLQNEINRLEKQAFLDQNADRASRTFESTSASRRQSD
KYSFORFYTSUNQEATSHKSERQOQNUEKCPBAGQTTSQNFFVPPTFKSVGNPVAR
RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA
QKIEEYSQQLEGITNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT
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Eutheria;
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Primates;
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n clone RP11-40020 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 500; DB 9;
Pred. No. 1.5e-256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-760M1 is at 92594 in this sequence.
The true right end of clone RP11-72P19 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr13
RP11-40020 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wi only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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19644. .1987
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/note="MIR repeat: matches 37963. .38254
                                                                                                                                                                                                                                       /note="MIR repeat: matches 3. 27150. .27653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3896.
                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 2154.
26938. .27096
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                                                                                                                                                                                                                                                                                                                                        26245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER46C repeat: matches 1. .286 of consensus"
18986. .19294
                                                                                                                                                               28522. .28891
/note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23342. .23651
/note="AluSg1 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches
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                                                                     'note="AluSx repeat: matches 1.
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note="L2 repeat:
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                                                                                                 .36415
                                                                                                                                                                                                                                                                                                                                                                                     .26109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 2554.
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                        22.
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                                                                                                                                                                                                                 .1644 of consensus
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62008 .62
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59350. .59
                                                                                                                                                                                                                                                                                                                                                                      /note="30
57357. .57
              /note="TIGGER1 repeat: matches 46. .1586 of consensus"
64386. .64694
                                                                 /note="TIGGER1 repeat: 62566. .62865
                                                                                                                                                                                                                                /note="AluSq repeat: matches 129. .313 of consensus" 59992. .60223
                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 82. .262 of consensus" 58260. .58389
                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. 57331. .57390
                                       /note="AluSq repeat: matches 1.
62866. .64385
                                                                                                                                                 /note="AluJo repeat: matches 85. .299 of consensus"
61036. .61144
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1MB6 repeat: matches 5822. .6172 of consensus"
55685. .55949
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1.
54179. .54511
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/note="AluSq_repeat: matches
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52204. .53009
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49168. .49212
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47477. .47873
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47067. .47365
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restriction digest data."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1.
                                                                                                         note="Alu repeat: matches 261.
                                                                                                                                                                                                                                                                                                  note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="CpG island"
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                                                                                                                       AluY repeat: matches 1. .129 of consensus" .62363
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72873. . 73249
/note-"MER31-internal repeat: matches
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/note="Allub repeat: matches 1. .299 of consensus"
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/note="11 copies 2
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/note="L1PB2 repeat:
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/note="TIGGER1 repeat: matches 65068 . 65395
/note="LIPB2 repeat: matches 54 65396 . 65569
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/note="MER21B repeat: matches 548. .680 of
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/note="10_copies 4 mer tgtg 82% conserved"
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70957. .71267
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AC079761.1 GI:10047966
HTG; HTGS PHACET
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Submitted (10-SEP-2000) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing
Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of Homo sapiens clone Unpublished
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Mammalia; Eutheria; P
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Waterston, R.H.
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Dederich, D., Thomas, S., Okwoon, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeed, M.P., Mei, G., Moore, S., Morgan, M., Morrits, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlingson, A.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Norres, Suhmission
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                                                                                                                                                                    Submitted (17-MAY-2000) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA On Sep 12, 2001 this sequence version replaced g
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Center: Baylor College of Medicine Center code: BCM
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SEQUENCE, 5 unordered
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                                                                                                                                                                                                                                                                                                                                             11492 bp
Sequence 3 from Patent WO0129266.
AXII9933
                                                                                                                 Hudson, T.J., Engert, J. and Richter, A.
Identification of arsacs mutations and methods of use therefor Patent: WO 0129266-A 3 26-APR-2001;
MCGILL UNIVERSITY (CA); Hopital Sainte-Justine (CA)
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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NOTE: This is a "vorking draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51417
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                     3599
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87026
136729
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168815
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Chemistry: Dye-primer Bodipy: 37% of reads
Chemistry: Dye-terminator Big Dye: 63% of reads
Chemistry: Dye-terminator Big Dye: 63% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 175525 bases at least Q30
Consensus quality: 179254 bases at least Q30
Consensus quality: 181014 bases at least Q20
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/db_xref="taxon:10000"
/clone="MGS3-342I16"
32907 c 34252 g 5516
                 /organism="Mus musculus"
/db_xref="taxon:10090"
2280 c 2387 g 3220
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100.0%; Pr
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174140: contig of 5226
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168814: contig of 8772 bp in length
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-OCT-1999) Genome Centre, 1650 Cedar Ave., Montreal, QC H3G 1A4,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GSSEGKMALKKIKWVPACKERPNYPGSLVWKGDLCHLCAPPMCDAAHAVLVGSSLP
LVESVHYNLEQALSIETSKPTINAVLKHEKTVVDWYTSKTFSDEDYYQFGHILLEIYGF
MHDHLSEGKDSFKALKFPWVWTGKRFCPLAQAVIKPTHDLDLQPYLYNVPKTMAKFHQ
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ENTRUPIYHSNAFSKLWKFDHSCYCDIKVDDLNDLLEDSVEPIILVEDIPMKTAA
TECSFMIDMRNMDIRENLLDFGMAACHGPALWSFNNSEFSDDFLNITTRLGESLKRG
EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMEDPNINHISKHIKDRSNPGIKINWSK
QKRLRKFPNQFKFIDVFGCQLFLAVBAPYSVNGTLFRLSFFTQQEAKVSEVSSTCY
UTADIYSLVDDESLCGHRLIETGSVNSMYLKYLKIETTNPSLAQDTIIKERKYCPSK
TADIYSLVEDESLCGHRLIETGSVNSMYLKYLKIETTNPSLADDTIIKTBKKVCPSK
KEIWKTDTKGRWNTTEMRHVIVKAYLQALSVLRDLAIGGELTDYTYYAVWPDPDLVHD
DFSVICKGFYEDIAHGKGKELTRVFSDGSMWVSMKNVRFLDDSILQRKDVGSAAFKIF
                                                                         ALNAPYLSYLKEAAKLMKTCSSSNKKLPTDYPKSSCILQITYEEEFHHYFRRIADLQSP
LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTYDCTTWLICTCMDTGEALKFSLNESG
                                                                                                                                                                                                                                                                                                                                                                                                                                      TDTSEKEKRIIQELTIFKRINHSSDQGISSYTKLKGCKVLDHTAKLPTDLRLSVSVID
SSDEATIRLANMLKIEKLKTTSCLKFVLKDIGNAFYTQEEVTQLMLWILENLSSLKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLFDEMPLIPRTLLNEDQTCVELIRLRIPSVVILDDETEAQLPEFLADIVQKLGGIVL
                                                  {\tt RRLGLVPCGAVGVLLHETQEQKWTVKPHIGEVFCYLPLRIKTGLPIHINGCFAVTSNR}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF31263.1"
/db_xref="GI:6907044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="sacsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MNTFWPGRELVVQWYPFSEDKRHPSLSWLKMVWKNLYIHFSEDL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
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Genome Res. 8 (10), 1022-1037 (1998 99018115
                                                                                                                  and Hood, L.E.
Complete genomic sequence and analysis of the
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 39760)
Lee,I.Y., Westaway,D., Smit,A.F.A., Wang,K., Seto,J., Chen,L., Lacharya,C., Ankener,M., Baskin,D., Cooper,C., Yao,H., Prusiner,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus long incubation prion protein protein (Prnd) genes, complete cds.
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U29187
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LDPNEMRTVKRVVSGLFKSLQNDSVKVRSDLENARDLALYLFSODGKLVKSSLLVFDD
APHYKSRIGGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLFRPLLSSILEEQLDE
ETPKVCQFGALCSLQGRLQLLLSSEQFTFGLIRIMKHENDNAFLANEEKA IRLCKALR
EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL
ALAMTLKSATDNILSDTSYLLAMLGCNDIYRISEKLDSLGVKYDSSEPSKLELPMPGT
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RLKHLLLEIGFRLLYYLODETANLYHCLVDADITVSYVTPADVRSELMTTSSPDTNCHI
GKLECRLOQTNLKLEHSLKLLVDYCFKDAEESSFEVEGLFLLTTLDSVLOIPDGKREK
ELTTYHELIPSRKDLEMNTLYLKYSSVLLNCKVAKVFDISSFADLLSSVLPREYKTKN
CAKWKDDFDASESWLKNAWHFISESVSVTDDQEEFKPAFDVIVDLIKDMALLPGTRETV
STSQLVVPEGDVLIPLSLMHIAVFRHAQSDKVTHALMKAGCIOLALNKICSKDSALVE
STSQLVVPEGDVLIPLSLMHIAVFNYQTSTFRTEKLMENDFEALLMYFNCNLSHLMSODDI
LLSCHTANIDSPASILKAVHYMYQTSTFRTEKLMENDFEALLMYFNCNLSHLMSODDI
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TACIIIKLENFIQQKV"
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MDLLSGNFLKELSLIFFLQFBRAPAEY IRFPQYQEVNGTLPFLIKFNGAQVNRKFKQC
DVLQLLWTSC DILPEKAFNLSIKGBEGSDLAPOEQLEQVLNMLNVNLDPPLDKVING
RNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRGVAFVMVEDGWKLLKPEE
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GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH
VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT
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SIPPLFSGKESHKSPSTKHHSPRKLKVNALPEILKEVTSVVEQAWKLPESERKKIIRR
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YEVLGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLASIEEPSEIKEQLFEK
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QVSEISSVPSSDRMVQNLLDKLRSDGAELLMFLNHMEKISICEIDKATGGLNVLYSVK
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FHLNFEAAPYLYQLPNKYKNNFRELFESVGVRQSFTVEDFALVLESIDQERGKKQITE
ENFOLCRRIISEGIWSLIREKRQEFCEKNYGKILLPDTNLLLLPAKSLCYNDCPWIKV
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7.100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-AUG-1999) Department of Molecular Biotechnology, University of Washington, Box 352145, Seattle, Washington
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5572..5712
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                                                     complement(7213. .7437)
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complement(5371..54
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1751.
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                                                                                                           /product="long incubation 6205. .21675
                                                                                                                                                                                                                                                                                                                                                             complement(5241.
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/rpt_family="B4"
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1874. .1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="84"
1857. .1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="strain=I/LnJ"
complement(1, .167)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="ORR1B"
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                                                                                                                                                                                                                                                                    _family="81_MM"
                                                                                                                                                                                                                      .6251
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                                    .7756)
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Seattle, Washington
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YYRPVDQYSNQNNFVHDCVNITIKQHTVVTTTKGENFTETDVKMMERVVEQMCVTQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1_MM"
18517. .1861"
                                                                                                                                                                                                                                                                  KESQAYYDGRRSSSTVLFSSPPVILLISFLIFLIVG"
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complement(11592. .11651)
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                                                                                                                                                           complement(24414.
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                                                                                                                                                                                                                                                      complement(22278.
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                                                                complement(27289.
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1, 16870
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. 27520
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. .17460
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. .27833
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REFERENCE
AUTHORS
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AUTHORS
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ORGANISM
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Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domaine Vilvert, Jouy en Josas 78352, France Location/Qualifiers
                                             2 (bases 1 to 10334)
BOLOTLI,A. Wincker,F., Mauger,S., Jaillon,O.,
Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
Direct Submission
                                                                                                                                      1 (bases 1 to 10334)
Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K.,
Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
The Complete Genome Sequence of the Lactic Acid Bacterium
Lactococcus lactis ssp. lactis IL1403
Genome Res. 11 (5), 731-753 (2001)
                                                                                                                                                                                                                                                Lactococcus lactis subsp. lactis.
Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                               complete genome.
AE006329 AE005176
AE006329.1 GI:12723880
                                                                                                                                                                                                                                                                                                                                                           AE006329 10334 bp DNA linear BCT 14-MAY-2001 Lactococcus lactis subsp. lactis IL1403 section 91 of 218 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 100.
22; Conservative
                                                                                                                                                                                                                                    Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon 2b; long form of exon 36212. .36751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MLT2CB"
complement(28530. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(GGA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MLT2D" 27819. .27910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="prion-like protein"
35130. .35341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36205. .37472
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/note="intergene exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="exon 2a; short form of exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="prion-like gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ._family="MLT1B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family-"L1ME3A"
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100.0%; Pred. No.
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to HW		/yene- yjnu /notee-m1172471" 2630. 3967	CDS
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ista 11		/gene="yjhC" /note="L172073" 22502513	CDS
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/Translation "MVNIYLVRHGKING EKGIKFDRAYSSDSGRTIQTMGFILANS DGVLPRIFTETCHHHTDERPPDEVIANA SEAKGAKNIVIVSHGMTIGTFVKLAHPE SYREIGSEKLAKK" 53066052	gene	/COGON_STATE=1 /transl_table=11 /transl_table=11 /product="HYPOTHETICAL PROTEIN" /protein_id="AAK05043.1" /protein_id="AAK05043.1" /db_xref="GI:12723882" /translation="MTLKTFFNFTRIQTLPAALLSPIAGCLFAFWYFGSFHFWPTLLF FTGIAGTHFUGARWINGARIDDEVERUNTIDAKSINDETAINGTAILATURGY PTGIAGTHFUGARWINGARIDDEVERUNTIDAKSINDETAINGTAILATURGY	
start=1 _table=11 t="phosphog1 n_id="AAK050 f="GI:127238		/gene="yjhb" /note="FVIDENCE BY HOMOLOGY BIO15.01 HYPOTHETICAL. General. there are three paralogs in L.lactis. 23% identical to putative 1.4-dihydroxy-2-naphthoate octaprenyltransferase of B.subtilis."	
/note="L174407" 46145309 /gene="yjhF" /note="EVIDENCE BY HOMOLOGY	CDS	complement(11552096) /gene="yjhB" /note="L171002" complement(11552096)	gene CDS
/gene="yjhE" /note="EVIDENCE BY GENEMARK /codon_start=1 /trans1_table=11 /product="UNKNOWN PROTEIN" /protein_id="AAKO5046.1" /db_xref="gi:12723885" /translation="MAYKVBFKDVETVG TYPAHEKADEVALFEKILLEERNLKFSA EKYGQEGKKFKRAVGIKLSVGMEIPKEL 46145309 /gene="yjhF"	gene	TEIN"  2.1"  1.1"  2.1"  INTERPOLITATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH	
/gene="yjhE" /note="L173848" 40674546	CDS	711129 /gene-"yjhA" /note-"sylDENCE BY GENEMARK BIO16.01 Unknown"	CDS
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K BIO16.01 Unknown"

VGLETSPVADSLAGLRANEARYFWNKYKFEYL SAKILEVAIYENDELYWPEFYYEDGMVLNLLY ELEGKFKFARQRSKLAGEIRGSYFTIKQEWL"

BIO06.09 Glycolysis"

mutase (EC5.4.2.1)"

MFNTIGRAQGWSDTPLTAAGEQGIIELGLGFK NSDNEGIPYTYDKRIREWCFGSPDGGYDGELF NAIFENDYAGMAEPWEKLSGRIMDGFTDIAKE PELPRPHGLDNGSVTHLSFEDGKFTIGKVGDM

Y BIO03.02 Murein sacculus and is corresponding enzyme mediates

ne carboxypeptidase (EC

VLLIIGALGFILITNDKSNSTNESAKKTSISS SPKDEMNEPILATWGIQVDQRIASAVQQFLAA YVQAEMNGQGTVNSSGNPISEEEAIKNVQTYS YAKQVAAIAPKYGFVLREPEGKKAETGIGYED LLPA"

K BIO16.01 Unknown" VALFIYSYSEMIKVLLVHNNFFSQFFNNLSTN LIFLLLKFWRFTFILLEIISALLIIDYAILFI KDSNLL"

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              Direct Submission
Direct Submission
Submitted (21-OCT-1997) National Institutes of Allergy and
Triectious Diseases, National Institutes of Health, NIH Campus,
                                                                                                                                                                                              Fidock, D.A., Nomura, T., Talley, A.K., Cooper, R.A., Dzekunov, S.M., Ferdig, M.T., Ursos, L.M.B., bir Singh Sidhu, A., Naude, B., Deitsch, K.W., Su, X.Z., Wootton, J.C., Roepe, P.D. and Wellems, T.E. Mutations in the P. falciparum digestive vacuole transmembrane protein PfRT and evidence for their role in chloroquine resistance
                                                                                                                                                                                                                                                                                                                                                                                Su,X., Kirkman,L.A., Fujioka,H. and Wellems,T.E. Complex polymorphisms in an approximately kDa protein chloroquine-resistant P. falciparum in Southeast Asia
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4 (bases
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FILPKSMTEADLAVFSNLVKERLVGKKVIDIHYTLRTEIPQIVQRYFKVTSEVLQLFE
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/gene="grpE"
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/db_xref="GI:12723889"
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Direct Submission
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/gene="o1"
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GLDIDDSEEAKKDFETLKAEYEGLCKVIKDVLHEKVEKVVVGQRITDSPCVLVTSEFG
WSANMERIMKAQALRDNSMTSYMLSKKIMEINARHPIISALKQKADADKSDKTVKDLI
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VEDVTEELENAEKKKERKKKIHTVEHEWEELNKQKELWKKEEEVTNEEYASFYKS
LTNDWEDHLAVKHFSVEGQLEFKALLFIPKRAPFDMFENKKKNNIKLYVRRVFINDD
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ENYKKFYEQFSKNLKLGIHEDNANRTKITELLRFQTSKSGDENIGLKEYVDRMKENQK
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NNKKLIKKNNHLISDISONSKEDSNKYKEKKKIKEKEKIKKEJDEEVTENNIDDK
NYTYNRDDEINDIESONSSONESIGEKPLDVHVKLATKGINYGVAAMPGEGQAIAGV
QKGKRIPRRGEVGLSAEAIENFESLGYVMSGSRHKRMNAIRMRKENQVYSAEEQRALA
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EKKKKKKRRSNIIIKGDSNSIRKSNSNSTRKSNSNSTRNSIRKSYNSNNKNHRKSRSY
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DETNEKLGRGTKIILHLKEDQLEYLEEKRIKDLVKKHSEFISFPIKLYCERQNEKEIT
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IRYESITDTQKLSAEPEFFIRIIPDKTNNTLTIEDSGIGMTKNDLINNLGTIARSGTK
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/rpt_unit=gkattbdtyttt
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                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSVLGIDIGNDNSVVATINKGAINVVRNDISERLTPTLVGFTEK
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KIINANVLRIISDNTAVALDYGMYRMEDFKEDMGSLLVFVNIGYANTCVCVARFESNK
CEILCDIADSNLGGRNLDNELIKYITNIFVNNYKMNPLYKNNTPELCPMGTGRLNKFL
VTSTASDQONGINNKVRIKLQEVAIKTKVAKOLNEASIHVECLYEDLDCGGSINRET
FEELCSNFFIJTKLKHLLDTALCISKVNJQDIHSIEVLGGSTRVPFIQNFLOQYFOKPL
SKTLIADESIARGCVLSAAMVSKHYKVKEYECVEKVTHPINVEMHNINDASKSNVEKL
YTRDSLKKKVKKIVIPEKGATYNTKSVIKKSKDEKKKDDKTBDKGEKKDAKOQONDDKDQ
TNDNNNEKDTNDKKEKNNETNSPNKTELKKGEEGKVQTCYTTIPITILLAQGSYSSK
DIRNFSEQEINMOHSDLLEGERLKHLMELETIIYESRSKLNGIYKNFVMDDERDRILL
DIRNFSEQEINMOHSDLLEGERLKHLMELETIIYESRSKLNGIYKNFVMDEERDRILL
DIRNFSEQEINMOHSDLLEGERLKHLMELETIIYESRSKLNGIYKNFVMDEERDRILL
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/gene="o2"
complement(9741.
/gene="o2"
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16000. .1856
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HHISYLGIKPKRFTVEWVEANKERERAENTNPITRYLDRRRKERGPHWILEDFLPSHP
CYLHNSKYHHDTELLRKMEEEAAEKEAESEEQEEEEEDITESEDDDN"
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EKEVKDVDKKHLELKEKLKMMKSSVSKONDSMNKUEIVQLAKMSDREKTREEIKKRLE
KYKREHKIYDGDESEDDEGEIDNKYFKNKNNLICESKNDEGHDNKYFKKKK"
complement(9741. 10358)
                                                                                                                                                      /gene="cg3"
complement(19529.
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complement(11754. .12377)
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complement(11754. .12377)
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IPKLEKNIEVVSHLKENVNVDYTYMVPKPVVIPIEVPILKFRDHFKIIPIRKKIIPVI
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ITQCSNKPSDESQNI INRTTKFLNNI NSLQEQEKNKPLY EPPVYTLNDI EAEFNEVTQ
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/product="CG3"
                                                                                                                      /gene="cg3"
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                                                                                                                                                                    AL Submitted (04-7UI-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 6, 2001 this sequence version replaced gi:14575107.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP
                   was generated from part of bacterial cione contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL157832 130192 bp DNA linear PRI
Human DNA sequence from clone RP11-109A6 on chromosome
http://www.sanger.ac.uk/HGP/Chr10
                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                          database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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DICPOELEKOJIVIEKIHKKYGDIITPIFISYDPOROJVAOJNYYCKSFSPKLIGLTG
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FLDFFGKNATTSEMVDKISEYIDDHMNKHKDYPKIQLAYKHKKKKKKKKKKKK
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join(23488. .23578,23748. .24016,24180. .24352,24522. .2/
24816. .24887,25011. .25086,25192. .25274,25401. .25451,
25589. .25645,25788. .25880,26075. .26119,26257. .26311,
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/note="PfCRT; detected by antibody"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="THE1B repeat: matches 1. .364 of con
THE1B repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2133. .2433
/note="AluJo repeat: matches 1. .298 of consensus
AluJo repeat: matches 1. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2654. .2838
/note="L2 repeat: matches 2320. .2502 of consensus
/note="L2 repeat: matches 2320. .2502 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1MC/D repeat: matches 5198. .5398 of consensus
L1MC/D repeat: matches 5198. .5398 of consensus"
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AluJb repeat: matches 3. .288 of consensus"
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L1ME3 repeat: matches 5718. .6031 of consensus"
                                                                                                                                                          MLT1A1 repeat: matches 1.
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/note="Llm4 repeat: matches 3184. .3266 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1MC/D repeat: matches 4632. .4649 of consensus"
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L1MB3 repeat: matches 5893. .6145 of consensus"
910. .1194
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/db_xref="taxon:9606"
                        /note="L1MC4 repeat: matches 7896. .7976 of consensus
.1MC4 repeat: matches 7896. .7976 of consensus"
                                                                                                                                                          /note="MLT1A1 repeat: matches 1. .365 of consensus
#LT1A1 repeat: matches 1. .365 of consensus"
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                                                                                                   'note="L2 repeat: matches 2583. .2625 of consensus"
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                                                                                                                                                                                                                                                                                                                                                             6. .4161
te="L1M4 repeat: matches 4957. .5204 of consensus
repeat: matches 4957. .5204 of consensus"
                                                                                                                                                                                                              ). .4576
:e="L1M4 repeat: matches 5191. .5310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e-"LIM4 repeat: matches 4741. .4957 of consensus repeat: matches 4741. .4957 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i. .3357
se="LlM4 repeat: matches 3184. .3479 of consensus"
                                                                                                                                                                                                                                                                                      e-"AluJb repeat: matches 1. .280 of consensus b repeat: matches 1. .280 of consensus"
                                                                                                                                 .11650
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                                                                                                                                                                                                                          /note="33 copies 4 | 28849. .28950 /note="3 copies 34 |
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/note="MLTIH repeat: matches 51. .344 of consensus MLTIH repeat: matches 51. .344 of consensus 16552. .16670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="11 copies 10 mer ggagaggga 63% conserved"
28029. .28132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1M4 repeat: matches 3237. .4327 of consensus L1M4 repeat: matches 3237. .4327 of consensus" 18030. .18355 /note="L1M3 repeat: matches 7416. .7739 of consensus L1M3 repeat: matches 7416. .7739 of consensus L1M3 repeat: matches 7416. .7739 of consensus" 18553. .18708
                                                                                                                                                                                                                                                                                                                              28017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 16. .207 of consensus
MIR repeat: matches 16. .207 of consensus"
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L1MC5 repeat: matches 7800. .7901 |
22715. .23147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1ME2 repeat: matches 6039.
L1ME2 repeat: matches 6039. .6122
22588. .22685
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16584. 16663
/note="MLT1H repeat: matches 456. .535 of consensus"
16680. .16875
/note="Alusx repeat: matches 30. .225 of consensus"
           note="Charliel repeat: matches 2498. .2729 of consensus"
32612. .32900
                                                                                                           /note="3 copies 34 mer 80% conserved"
31353. .32326
/note="L1PB2 repeat: matches 5174. .6152 of consensus"
L1PB2 repeat: matches 5174. .6152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1M4 repeat: matches 3760. .4703 of consensus"
25400. .25587
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23171. .24090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12715. 23147

'Moote="LIME2 repeat: matches 5711. .6143 of consensus IME2 repeat: matches 5711. .6143 of consensus"

23171. .24165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1MB3 repeat: matches 5673.
19815. .19895
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18838. 19420
/note="LIME2 repeat: matches 5313. .5944 of consensus
LIME2 repeat: matches 5313. .5944 of consensus"
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'note="L2 repeat: matches 2543. .2750 of consensus 2 repeat: matches 
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                                                                                                                                                                                                                                                                                                              2 (bases 1 to 163721)

2 (bases 1 to 163721)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Cook, A., Cook, P., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., DeArellano, K., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Tanderson, B., Landerson, C., L
                                                                                                                                                                                                                                  Viel, R., Vo, A., Wilson, B., Wu, X., wyman, U., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                              Submitted (18-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-368E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC099718 163721 bp DNA Mus musculus clone RP23-368E4, WORKING
                                             nttp://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_FULLTOP
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   Center: Whitehead
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/note="Charliel repeat: matches 2488. .2498 of consensus 2906. .32950
/note="Charliel repeat: matches 1822. .1868 of consensus Charliel repeat: matches 1822. .1868 of consensus Charliel repeat: matches 1822. .1868 of consensus 34137. .34372
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/note="8 copies 10 mer ccacacaca 71% conserved"
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AluSx repeat: matches 1. .304 of consensus"
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AluSx repeat: matches 1. .308 of consensus"
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                                  --- Genome
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                                     Center
Institute/ MIT Center for Genome Research
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BASE COUNT
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                                                                                       Local Similarity 100 hes 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 163000; agarose-fp
Insert size: 163221; sum-of-contigs
Quality coverage: 8.7 in Q20 bases; agarose-fp
Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.68731 Consensus quality: 161403 bases at least Q40 consensus quality: 162593 bases at least Q30 Consensus quality: 162938 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L1768
Center clone name: 368_E_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25936 26035: gap of 100 bp
26036 132236: contig of 106 bp
132237 132336: gap of 100 bp
132337 163721: contig of 31385 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 1925: contig of 1925 bp in length
1926 2025: gap of 100 bp
2026 2677: contig of 652 bp in length
2678 2777: gap of 100 bp
2778 3978: contig of 1201 bp in length
3979 4078: gap of 100 bp
4079 25935: contig of 21857 bp in length
25936 26035: gap of 100 bp
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30666 c 30186 g
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/note="assembly_fragment"
132337. .163721
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2026. .2677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                         /note="assembly_fragment
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|. .1925
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                                                                                                            100.0%;
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                                                                                                       Score 21; DB 2; ; Pred. No. 4.5;
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e; 100% of reads
                                                                                          0;
                                                                                                                                   Length 163721;
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                                                                                          Indels
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RESULT 13 AC018633/c

	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL
Center: University of Washington Genome Center Center code: UNCC Web site: http://genome.washington.edu Contact: uwgchelpeu.washington.edu Contact: uwgchelpeu.washington.edu Contact: uwgchelpeu.washington.edu Center project name: chr-7 Center project name: chr-7 Center project name: chr-7 Center clone name: djs1 (RP11-16G1) Center clone name: djs1 (RP11-16G1) Center clone name: djs1 (RP11-16G1) Center clone pame: djs1 (RP11-16G1) Center clone name: djs1 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP11-16G1) Center clone pame: djs2 (RP1	ACO18633  ACO18633  ACO18633  ACO18633  ACO18633.2  GI:6729063  HTG.  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 169234)  Kaul,R.K., Yu,J., Wong,G.KS., Magness,C.L., Green,E.D., Green,P.  Large-scale MCD Mapping and Sequencing of Human Chromosome 7  2 (bases 1 to 169234)  Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.  Direct Submission  Submitted (15-DEC-199) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  3 (bases 1 to 169234)  Direct Submission  Submitted (21-JAN-2000) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA  On Jan 21, 2000 this sequence version replaced gi:6579285.
	FP 2055.00 5487.00 1913.00 1508.00 12901.00 1004.00 529.00 10358.00 3805.00 1674.00 2228.00 3051.00
1175.00 11874.00 12269.00 22269.00 2243.00 1325.00 4449.00 4449.00 10132.00 1676.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11776.00 11	Seq 2061.00 5270.00 11893.00 11491.00 119322.00 1992.00 1992.00 1992.00 10526.00 10526.00 3819.00 2170.00 2170.00
	FP 8954.00 7648.00 7648.00 838.00 4399.00 4140.00 660.00 3053.00 5075.00 6909.00 1911.00 3635.00
	Seq 8687.00 7660.00 7556.00 801.00 4094.00 643.00 643.00 5106.00 6771.00 1874.00 1874.00

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SOURCE
ORGANISM
                                VERSION
KEYWORDS
                                                           DEFINITION
ACCESSION
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AF034998
LOCUS
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                                                                                                                                                 Db 133656 AAAATCTTTATATACATTTTT 133636
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Hyphantria cunea
                                                         AF034998 1295 bp
Hyphantria cunea immune-related
AF034998
                                               AF034998.1
                      fall webworm moth.
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392. 494
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10137. .10423
                                                                                                                                                                                                                                                                                                                     complement(6970. .7082)
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/note="GenBank Accession Number: G00158"
                                                                                                                                                                                                                                                                                                                                                                           complement(5307. .5594)
/rpt_family="Alu"
5847. .6152
                                                                                                                                                                                                                                                                                                  complement(7545. .7634)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3252. .3702)
/rpt_family="MLT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
complement/conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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1. .169234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="GenBank Accession Number: G12923"
2594...2876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2210. .2373)
/standard_name="sWSS2626"
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6 (cooke, P., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., Dearellano, K., Gage, D., Galagan, J., Gardyna, S., Gooke, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pleare, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lancers, E., Landers, T., Leboczky, J., Levine, R., Liu, G., Mactean, C., Landers, T., Leboczky, J., Levine, R., Liu, G., Mactean, C., Landers, T., Leboczky, J., Levine, R., Liu, G., Mactean, C., Maccanthy, M.,
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 57205)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo Sapiens Chromosome 15, Clone RP11-577014
Unpublished
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1 (bases 1 to 1295)
Shin,Sw., Park,S.S., Park,D.S., Kim,M.G., Kim,S.C., Brey,P.T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE SAMPLING.
AC107995
AC107995.1 GI:18308723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC107995 57205 bp DNA linear Homo sapiens chromosome 15 clone RP11-577014 map 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-NOV-1997) Insect Resources Lab., Korea Research Institute of Bioscience and Biotechnology, P.O. Box 115, Yusong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Shin, S.W., Park, S.-S. and Park, H.-Y.
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Insect Biochem. Mol. Biol. 28 (11), 827-837 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99035790
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GQDXVQHPVVIQQEDNQQVPRNRDIKGGETEQRTIKQTFGEELGSAKNINQSDIAQES
QNKEMQAVIDSOVFQAKBCEESKKFTABEMKFJQVAQHFDGSQKLDKNIDHVRVGIDGD
QKVQLSTEKNVKGQQTEKSIQVQQTNDSQQAKKQVNVPLPYLKQ"

a 246 c 255 g 322 t
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/protein_id="AAD09279.1"
/db_xref="G1:4090964"
/translation="MYVLLAIVCLVSTASAKDLTVGREGGSLKFEQNFTASPTIWRQA
/translation="MYVLLAIVCLVSTASAKDLTVGREGGSLKFEQNFTASPTIWRQA
KTVTFNVSDFEYITQVAIVDRREDKDGEAVIIEGGENHKNVTIELKSPAVFRGFDFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Hyphantria cunea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-JAN-2002) Whitel Research, 320 Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback, Severy,P., Spencer,B., Stange-Thomann,N., Stojanovio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing reads that have not been assembled into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      will be sequenced to
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Center clone name: 577_0_14
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110 43061: contig of 752 b

62 43161: gap of 100 bp

62 43892: contig of 731 bg

33 43992: gap of
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2 20642: contig of 7
3 20642: gap of 10
43 21361: contig of 3
7 161: gap of 5
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22 32321: gap of 100 bp

12 33044: contig of 723 b

5 33144: gap of 100 hr

5 33863
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5 44824: gap o
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36453: gap of 1
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30695: gap of
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24713: con
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17185: con
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1460: gap of 72
42209: Contig of 72
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18872: contig
72: gap of
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21361: contig of 719 bp in
61: gap of 100 bp
22213: contig of 752 bp in
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ap of 100 bp
s: contig of 723 bp in length
725 bp in length
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Search completed: May 22, 2002, 08:30:10 Job time: 10700 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

9	8	7	6	5	4	ω	2		Result
19	19	23	35	500	500	500	500	500	Score
3.8	3.8	4.6	7.0	100.0	100.0	100.0	100.0	100.0	Query
1543	721	23	11493	12793	12793	12793	12793	12792	Query Match Length DB
23	16	22	22	22	22	22	22	22	BB
AAS83269	AAT35105	AAH20130	AAH20175	AAH20182	AAH20179	AAH20178	AAH20174	AAH20176	ID
DNA encoding novel	Down-regulated sen	Human spastin ORF	Mouse spastin nucl	Human mutated spas	Human mutated spas	Human mutated spas	Human spastin nucl	Human mutated spas	Description

20-OCT-1999;

99US-0160588

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22	22	22	22	22	22	22	21	19	19	22	22	22	22	21	24	20	22	22	22	24	22	24	20	22	21	21	22	23	22	22	22	24	23	18	22
AAI92739	AAK60614	AAH02487	AAH84736	AAH93422	AAS10065	AAS63514	AAA06306	AAV58543	AAV61286	AAS28204	AAS28202	AAL32440	AAF28552	AAF22280	ABL34146	AAX06876	AAK91462	AAS40045	ABA16800	ABL33061	AAS45475	ABL34564	AAX84918	AAH54577	AAC39202	AAC47212	AAH53781	AAS87201	AAF55108	AAF55109	AAH12392	4	451	5	AAH72857
Human polynucleoti	Human immune/haema	Prostate tumour an	Human prostate-spe	Human prostate-spe	Human prostate tum	Human prostate cDN	Human immunogenic	8	cDNA sequence of p	Genomic sequence #	Genomic sequence #	Human SNP oligonuc	Genomic fragment #	BAC containing rep	Human immune syste	Caenorhabditis ele	Human digestive sy	Genomic sequence #		Human immune syste	Chemically pretrea	Human metastasis a	Rat brain specific	S. epidermidis gen	Arabidopsis thalia	Arabidopsis thalia	S. epidermidis ope			Nucleotide sequenc	Human cDNA clone (	Human immune syste	Drosophila melanog	ylococcus	Human cervical can

## ALIGNMENTS

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RESULT
AAH20176
Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                            CDS
                                                                                                                                                              Homo sapiens.
Synthetic.
                                                                                                                                                                                                    abnormal neuronal lipid storage; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                AAH20176;
                                                                                                                                                                                                                                                                                                                                                                        AAH20176 standard; DNA; 12792
                                                 26-APR-2001.
                                                                          WO200129266-A2
                                                                                                                                                                                                                                                                                             Human mutated spastin nucleotide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                       09-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in CG gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for assaying the presence of a nucleic diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC markers, to identify genetic disorders, as hybridisation probes or CC markers, to identify and express recombinant protein for CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC in which the corresponding protein is expressed. Diagnostic methods from CC in researt invention can be used to identify subjects having or at risk of developing a disorder associated with aberrant expression CC correction or spastin gene expression or activity. The present sequence is not given in the present specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 500; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12792 BP; 4163 A; 2256 C;
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    The present sequence is not given in the present
derived from the human spastin nucleotide sequence
ated on page 14.

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                   agtcattttagacgatgaatctgaagcacagcttccagaatttttagcagacattgtaca
                                                                                                 aactatactagaggaaggtcagacatgtgtggaactcattagactcaggattccatcgtt
                                                                                                                                                                                                                                                     tccatttgatgaaaacagaaatcacccatctgtttcatggcttaagatggtttggaaaaa
ag_ccattttagacgatgaatctgaagcacagcttccagaatttttagcagacattgtaca
                                                                                                                                                                           tctttatatacatttttcagaggatttgactttatttgatgagatgccacttatccccag
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)B; AAB97821.
                                                                           aactatactagaggaaggtcagacatgtgtggaactcattagactcaggattccatcgtt
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                                                                                                                                                                                                                                   tccatttgatgaaaacagaaatcacccatctgtttcatggcttaagatggtttggaaaaa
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100.0%; Pred. No. 4.7e-239;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
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                            gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or adding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                      The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to
                                                                                                                                                                                                                                                   chromosome 13q11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human spastin nucleotide sequence
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    have neuroprotective activities and

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                                            autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence encodes human spastin as given in the present invention.
                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                       09-AUG-2001
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Matches Query Match

500;

Conservative

0;

Mismatches

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Indels Length 12793;

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Gaps

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Local

Similarity

100.0%;

Score 500; DB 22; Pred. No. 4.7e-239;

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The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC diagnosis of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC antiphy of upper cerebellar vermis, absence of purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce CC antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC primers, as an antigen, identify and express recombinant protein for CC canalysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aboreant expression.
                                                                            of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence represents a mutated human spastin gene from the present invention.

N.B. The present sequence is not given in the present specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnos; reduced motor nerve velocity; hypermyelination of retinal nerve fibratrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation;
                                                                                                                                   Claim
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AAH20182
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AC AAH2
XC AAH2
XX
DT 09-A
XX
DE Huma

Human mutated

spastin nucleotide

sequence

SEQ

IJ

NO:15

09-AUG-2001 (first entry)

RESULT

AAH20182

standard;

DNA;

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No. 4.7e-239;
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CC The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13qll. (I) have neuroprotective activities and can be used in CC gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC diagnosis of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyslination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of putkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce CC markers, to identify genetic disorders, as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC analysis, characterisation or therapeutic use, or as markers for tissues the present invention can be used to identify subjects having or at risk CC of developing a disease or disorder associated with aberrant expression
                                      Query
Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin gene sequence -
                                                                                                                                                                                                                              N.B. The present seq
is derived from the
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                                                                                                                                                                                                                                                                                                                                    of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page -;
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                                                                                                                                               Sequence 12793
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Mismatches 0;
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Matches

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Similarity

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                                                                                                                                                                                                                                                                                                         Human; mouse; spastin; ARSACS; chromosome 13q11; identification;
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                                  SAINTE-JUSTINE
                                                                                                                                                                                     Location/Qualifiers
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           Richter A;
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The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, a trophy of upper cerebellar vermis, absence of purkinje cells and antisense nucleic acids, is useful as molecular weight or chromosome can markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression protein or spastin gene expression or activity. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
     20-OCT-2000; 2000WO-US29130
                                                                                                                                                                                                      Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
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P-PSDB; AAB97820.
                                                 26-APR-2001.
                                                                                WO200129266-A2
                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                               Human spastin ORF PCR primer SEQ ID NO:23
                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          AAH20130 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 8; 76pp; English.
                                                                                                                                  Homo sapiens
                                                                                                                                                                                      abnormal neuronal lipid storage; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11493 BP; 3599 A; 2281 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encodes mouse spastin as given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 gatttgactttatttgatgagatgccacttatccc
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                                                                                                                                                                       primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Senescence related gene; expression; inhibition; acceleration; tomato; Down-regulated senescence clone, SEND31 proposed full legth sequence.

strawberry; wheat; maize; rice; rape;

senescence; yield; protein content; quality; ed senescence; desiccant; ss.

delayed

Lycopersicon esculentum increased senescence; lettuce; cabbage; banana;

23-MAR-1995 WO9507993-A1 밁

AAT35105

œ

AAT35105 standard; cDNA;

21-NOV-1996

(first entry)

Qγ

Matches

Conservative

0;

Mismatches

0;

0

0

Query Match Best Local Similarity

4.6%;

Score 23; DB 22; Pred. No. 0.17;

Length 23; Indels

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Chromosome 13q11. (1) have neuroprotective activities and can be used in CC gene therapy and as a spastin polypeptide agonists. (1) their fragments CC or their complements can be useful for assaying the presence of a nucleic caid molecule in a sample. (1) is useful for assaying the presence of a nucleic caid molecule in a sample. (1) is useful for diagnosing or aiding in the CC diagnosis of an early onset neurodegenerative disease in an individual. CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, catrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (1) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome cc markers, to identify genetic disorders, as hybridisation probes or crimers, as an antigen, identify and express recombinant protein for cc analysis, characterisation or therapeutic use, or as markers for its companies of the present invention can be used to identify subjects having or at risk of developing a disorder associated with aberrant expression or activity of (1). The assays can be utilised to identify a subject having or spastin gene expression or activity. AAH20122 to AAH20173 represent specifically claimed primers which can be used in diagnostic mather the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to
Sequence
                                              methods from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene sequence
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(HOPI-) HOPITAL SAINTE-JUSTINE.
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  23
BP;
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7 A;
                                         present invention.
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3 G;
6 T; 0
  other;
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RESULT
AAS83269
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in plants including tomato, lettuce, cabbage, banana, strawberr wheat, maize, rice, rape or soybean. Delayed senescence may indirectly prolong the life of the plant, increase yield, increprotein content of fruits, improve quality of leafy vegetables,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAT35095-133 are senescence related genes a fragments which were used in the construct of the invention which modifies the expression of at least one senescence related gene. Using these constructs senescence may be inhibited or accelerated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drake
                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #19073.
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    31-MAR-2000; 2000US-0540217
                                           30-MAR-2001; 2001WO-US08631
                                                                                                                                      WO200175067-A2
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                              AAS83269;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAS83269 standard; cDNA; 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                        supplement;
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                                                                                                                                                                                                                          chromosome mapping;
upplement; medical ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721
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Smart CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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100.0%;
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Thomas H;
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                                                                                                                                                                                                                      imaging;
                                                                                                                                                                                                                      gene mapping; gene
naging; diagnostic;
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Pred. No.
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of in crop plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                      genetic of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                        disorder;
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08-DEC-1999;
21-DEC-1999;
14-MAR-2000;
                                                                                                                               14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                 AAH72857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics; forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess the discrete for genetic disorders.
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                                                                                                                                                         08-DEC-2000;
                                                                                                                                                                                                                                                                                                                  WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cervical cancer marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH72857 standard;
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hes 19; Conser
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99US-0169681.
99US-0171350.
2000US-0189315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pre-malignant condition; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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Pred. No.
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17;
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RESULT 11
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        07-JAN-1997;
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09-JUN-2000;
21-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostaric activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
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                                      30-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                  syndrome;
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2000US-0210600.
2000US-0220114.
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            97EP-0100117
                                                                                                                                                                                                                                                                        aureus
                                                                                                                                                      the sequence are included given in the 2221..2280
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                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and detecting
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                                                                                        "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering are included to maintain the received numbering are included to maintain the nucleotide numbering are included to maintain the nucleotide numbering are included to maintain the nucleotide numbering are included.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1051pp;
                                                                                                                                                                 "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                 #246.
                                                                                       specification
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17;
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melanogaster.

developmental

biology;

cell signalling;

insecticide,

gene;

SS

Drosophila melanogaster expressed polynucleotide SEQ ID NO 38018.

26-MAR-2002 ABL14512 ABL14512

(first entry)

23-MAR-2000; 11-JUL-2000; 23-MAR-2001; 27-SEP-2001 WO200171042-A2 Drosophila pharmaceutical; Drosophila;

2000US-191637P 2000US-0614150 2001WO-US09231

(PEKE ) PE CORP NY

JC,

Adams M,

Li PWD,

Myers

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                                                                  Matches
                                                                                Query Match
Best Local :
                                                                                                                                                                                             that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                    medium, prefer memory (RAM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) and proteins derived stored on computer readable medium and anti-S.aureus vaccines
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    the S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                               415 tattaaaaaatatattcat 433
Local Similarity hes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  the invention. The DNA sequences are recorded on a computer readable dium, preferably selected from a floppy or hard disk, random access mory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                   3365
                                                                                                                                                                                    readable medium
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                                                                  Conservative
                                                                                                                                                   BP;
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Pred. No.
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiarinflammatory; cancer; eye disease; arterioscilerosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy neurofibromatosis; rheumatoid arthritis; psoriasis; bowel di
Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                    01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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01-SEP-2000;
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19; Conservative
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                                                                   Piepenbrock C,
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       The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                     Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detecti and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                        11-JAN-2000;
02-MAY-2000;
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   The present sequence encodes a BASB119 polypeptide of Moraxella catarrhalis strain ATCC43617. BASB119 polypeptides and polynucleotides are useful for generating an immune response in an animal. The polypeptides may also be used as prophylactic agents of bacterial
polypeptides may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASB119; immune response; bacterial infection; genetic immunization; otitis media; pneumonia; sinusitis; nosocomial infection; invasive disease; hearing loss; fluid accumulation; antibacterial; s:
                                                                                                                                                                            Claim 13;
                                                                                                                                                                                                                                                                 New BASB119 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines against
                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB67488.
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                                                  invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, infection of the upper respiratory tract, or inflammation of the middle ear. The polypeptides or polynucleotides may also be employed as research reagents and materials for discovering treatments of and diagnostics for diseases, particularly human diseases. In particular, the polypeptides or polynucleotides are useful in the discovery and development of antibacterial compounds, or for diagnosing diseases, staging of the disease, determining the response of an infectious organism to drugs.
                                                                                                                                                                                                                                                                                              infections, particularly M. catarrnalis infections with the polynocleotides are useful in therapy or prophylaxis, particularly genetic immunization against these infections or diseases. These diseases include otitis media in infants or children, pneumonia in elderlies, sinusitis, nosocomial infections and children.
Sequence 513 BP; 173 A; 78 C; 111 G; 151 T; 0 other;
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Matches
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103
       104 ttgattgttcaatggtat 121
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TTGATTGTTCAATGGTAT 86
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Pred. No.
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Search completed: May 22, 2002, 08:35:42 Job time: 6562 sec

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US-09-020-956-66/c US-09-020-956-66/c Sequence 66, Application US/09020956 Patent No. 6261562 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: NILLIAN DAVIN C. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF INUMBER OF SEQUENCES: 178 CORRESPONDENCE ADDRESS: ADDRESSE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: WA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	Query Match Best Local Similarity 100.0%; Pred. No. 8.2; Matches 18; Conservative 0; Mismatches .0; Ind Qy 321 ctgaagcacagcttccag 338 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	US-09-600-776-10 US-09-600-776-10 Sequence 10, Application US/09600776 Patent No. 6326168 GENERAL INFORMATION: APPLICANT: Yamanouchi Pharmaceutical Co., Ltd. TITLE OF INVENTION: A novel potassium channel protein FILE REFERENCE: Y9903-PCT CURRENT APPLICATION NUMBER: US/09/600,776 CURRENT FILING DATE: 2000-07-21 PRIOR APPLICATION NUMBER: JP P1998-011434 PRIOR FILING DATE: 1998-01-23 PRIOR FILING DATE: 1998-01-23 PRIOR FILING DATE: 1998-12-04 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10 LENGTH: 3736 TYPE: DNA ORGANISM: Rattus sp. US-09-600-776-10	ALIGNMENTS	28 16 3.2 2156 1 US-08-321-356-3 29 16 3.2 2372 4 US-09-130-616-174 30 16 3.2 3450 2 US-08-714-916-63 31 16 3.2 3592 3 US-09-265-315-63 32 16 3.2 3592 4 US-09-265-315-63 33 16 3.2 3592 4 US-09-265-315-63 34 16 3.2 3592 4 US-09-265-315-63 35 16 3.2 3592 4 US-09-265-315-63 36 16 3.2 3592 2 US-08-469-537A-102 37 16 3.2 3906 2 US-08-164-292B-1 38 16 3.2 4060 1 US-08-164-292B-3 39 16 3.2 4060 1 US-08-164-292B-3 39 16 3.2 4060 1 US-08-164-292B-3 39 16 3.2 4060 1 US-08-164-292B-3 39 16 3.2 4060 1 US-08-164-292B-3 39 16 3.2 4060 3 US-08-845-623-1 39 16 3.2 4060 3 US-08-845-623-3 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 16 3.2 4060 3 US-08-845-623-7 39 17 18 18 18 18 18 18 18 18 18 18 18 18 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6262245
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, Jiangchur APPLICANT: Dillon, David TITLE OF INVENTION: COM NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mak1, Dav1d J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                               SEQUENCE CHARACTERISTICS:
                                                                                                          TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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TOPOLOGY linear
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                       STRANDEDNESS:
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Maki, David J.
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NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 66
LENGTH: 305
TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                              Sequence 5, Application US/08390162 Patent No. 5576192 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 1999-1
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COMPUTER READABLE FORM
                                                                                                             TITLE OF INVENTION: Prostogland TITLE OF INVENTION: Production NUMBER OF SEQUENCE: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                   APPLICANT: Ichikawa, Atsushi
APPLICANT: Narumiya, Shuh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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     COUNTRY: USA
2TP: 20005-3315
                                                                   STREET:
                                       STATE: D.C
                                                     CITY: Washington
                                                                               ADDRESSEE:
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o. 6329505
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Reed, Steven G
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                                                               E: Dunner
1300 I Street, N.W.,
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                                                                                              Finnegan, Henderson, Farabow,
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Pred. No.
                                                                     Suite 700
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SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:

MEDIUM TYPE: Flop COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible YSTEM: PC-DOS/MS-DOS

Release #1.0, Version #1.25

Floppy disk

FILING DATE: CLASSIFICATION: 435

APPLICATION NUMBER:

US/08/390,162

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Best Local
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                             FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 23-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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LENGTH: 2442 base pairs
                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 22-JUL-1996
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FILING DATE: 23-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ichikawa,
APPLICANT: Narumiya,
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PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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17; Conserv
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Pred. No.
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                      FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 30-APR-1992
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REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                  CLASSIFICATION:
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                                                                                                                FILING DATE:
                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
REFERENCE/DOCKET NUMBER:
             NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16, Application US/08392625
o. 5837485
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                                                                                                                                                                                                                                   D.C.
Y: U.S.A.
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                                                                                                                                                                                                                                                                                      E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2442 base pairs
                                                                                                                                                                                                                                                                                                                                                                        Kellner, Roland
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Engelke, Germar
Rosenstein, Ralf
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                                                                                                                                                                                                                                                                                                                                                                                                                     Wieland, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaletta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schnell, No. 5837485bert
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                                                                    US 07/876,791
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Pred. No.
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TELECOMMUNICATION INFORMATION:

202) 371-2600

TELEPHONE:

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                                                                                                          PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/876,791

FILING DATE: 30-APR-1992

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/784,234
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                            STREET: LIVU
CITY: Washington
STATE: D.C.
                              REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 31-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                CLASSIFICATION:
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nes 17; Conserv
                    TELEPHONE:
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ELEFAX:
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                                                                           Esmond, Robert W
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1100 New York Avenue,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Entian,
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                     202)
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ork Avenue, NW
                                                                                                                                                                                                               US 08/392,625
                                                 0652.0980004
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Pred. No.
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RESULT

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                                                    Matches
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Best Local :
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                                                                                                                                                                                                     TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,89
REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,193B
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CITY: Washington
STATE: D.C.
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574 TATTAAAAAATATATTC 558
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                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
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ZIP: 20005
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17; Conserv
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EDNESS: both
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1100 New York Avenue,
                                                                                                                                                                                                                                  (202)
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Kempter, Christoph
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                                                    Conservative
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                                                                  Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldstein &
e, Suite 600
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                                                    Mismatches
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                                                                            Length 8700;
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                                                     Indels
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RESULT 11
US-08-884-324-14
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                                                                                                                                                                                         Sequence 14,
Patent No. 6
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Patent No. 6060283
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 26 Matches 17; Conservative 0; Mismatches
                                                                          GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahi KURIMOTO
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8835 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                         3604 TTCTGGCCTGGCAGAGA 3620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patent In Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
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                               TITLE OF INVENTION:
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APPLICANT: Masahi KURIMOTO
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LOCATION: 1.8835
IDENTIFICATION METHOD:
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
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SYSTEM: PC-DOS/MS-DOS
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GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE OF INDUCING THE PRODUCTION OF INTERFERON-35
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PROPRICATION NUMBER: JP 18
APPLICATION NUMBER: 27-UN-1996
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: BROWDY AND NEIMARK
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TYPE: nucleic acid
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                                                                                                   IDENTIFICATION METHOD:
NAME/KEY: mat peptide
06828.27046
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                                                                             LOCATION: 26828..2704 IDENTIFICATION METHOD:
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20469..20586
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US-08-884-324-14

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RESULT 13
5432082-6/c;
Patent.No. 5432082
; Patent. Galeotti, Cesira; Palla, Emanuela; Raugei, Giovanni;
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; ANTI-SENSE: 1
US-09-025-580-19
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US-09-025-580-19/c
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NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                  Query Match
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APPLICANT: Su, Mi
APPLICANT: Fox, T
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|||||||||||||||||
10367 TTCTGGCCTGGCAGAGA 10383
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
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LENGTH: 37 base pairs
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Methods for Designing Inhibitors of
TITLE OF INVENTION: Serine/Thereonine Kinases and Tyrosine Kinase
NUMBER OF SEQUENCES: 37
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                                                                                                                             FILING DATE:
CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Fox, Ted
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Pred. No.
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Best Local Similarity
"~+~hes 16; Conserv?
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US-08-946-914-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TITLE OF INVENTION: EXPRESSION AND SECRETION VECTOR IN YEASTS, SUSSEUL FOR PREPARING HETEROLOGOUS PROTEINS NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:6:
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 60/028,093
FILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                   TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 449 base pairs
TYPE: nucleic acid
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gentz, Reiner L. APPLICANT: Ruben, Steven M.
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FILING DATE: 11-FEB-1991; 02-
APPLICATION NUMBER: 69,329
FILING DATE: 02-JUL-1987
                                TOPOLOGY:
                                               STRANDEDNESS:
                                                                                                                                                                                                       NAME: Steffe, Eric K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                     202-371-2540
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Pred. No.
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Query Match

3.28;

Score 16;

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Length 449;

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Search completed: May 22, 2002, 08:29:03 Job time: 6868 sec
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; ORIGINAL SOURCE:
; ORGANISM: PAG:
US-08-998-416-1092
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US-08-998-416-1092/c
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                                                                                                                             Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998.416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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Patent No. 6239264
GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1092:
SEQUENCE CHARACTERISTICS:
LENGTH: 677 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                                                          304 cattttagacgatgaa 319
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ZIP: 27709
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Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
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78;
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Minimum DB
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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2 AZ066617
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BG599717
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BH348265
BG593815
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AZ649875
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BF322199 MR0-AN008
BH025017 RPCI-24-3
BH126217 RPCI-24-3
BH126217 RPCI-24-3
AZ649875 IM0519B14
BB561400 BB561400
AZ066617 RPCI-23-4
AZ644393 IM050BN18
BH110525 RPCI-24-3
BF397419 UI-R-BS2-
BF397419 UI-R-BS2-
BF397419 UI-R-BS2-
BF397419 UI-R-BS2-
BF397419 UI-R-BS2-
BF397419 UI-R-BS2-
BG599717 EST504612
BG899484 EST515335
AW018508 fd58h04.y
BH348265 CCH230-120
BG593815 EST492493
AL396917 T3 end of
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## ALIGNMENTS

JOURNAL MEDLINE COMMENT REFERENCE AUTHORS RESULT 1
BE008891/c
LOCUS
DEFINITION
ACCESSION
VERSION SOURCE ORGANISM FEATURES KEYWORDS TITLE source 1 (bases 1 to 241)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
,M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL Tel: +55-11-2704922 Fax: +55-11-2707001 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research Shotgun sequencing of the human transcriptome with ORF Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. human. EST BE008891.1 BE008891 BE008891 241 bp mRNA linear CM4-BN0161-040400-132-d08 BN0161 Homo sapiens cDNA, Seq primer: puc 18 forward (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM4-BN0161-040 400-132-d08&t3=2000-04-04&t4=1) Rua Prof. Antonio 20202663 sequence tags Simpson, A.J. Proc. Natl. Acad. Sci. U.S.A. quality sequence start: 6 quality sequence stop: 241 Location/Qualifiers ∕organism≖"Homo sapiens" GI:8269124 Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, 97 (7), 3491-3496 (2000) mRNA sequence. expressed

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RESULT
BF326199
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-MRO&t2-MRO-AN0083-
169900-003-d10&t3-2000-09-16&t4-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                  primer: puc 18 forward
h quality sequence stop: 11.
Location/Qualifiers
                                                                                                                                                                                                                                                                        +55-11-2707001
                                                                                                                                                                                                                                                                                         +55-11-2704922
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                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="AN0083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone_lib="BN0161"
/dev_stage="Adult"
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Pred. No.
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COMMENT
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BH025017/c
ORIGIN
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                  BASE COUNT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_GSSs: RPCI-24-318E15.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 318 row: E column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , DNA sequence.
BH025017
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                                                                                                                                                                                                                                                                                                                 Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao, S., Nierman, W., Malek, J., Shatsman, S., A)
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-24
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Mammalia; Eutheria; Rodentia;
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                    229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      szhao@tigr.org
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                                        /cell_type="Spleen/Brain" /cell_type="Spleen/Brain" /note="Vector: pTAKBAC1; Site_1: BamH1; Site_2: BamH1; /note="Vector: pTAKBAC1; Site_1: BamH1; Site_2: BamH1; /note="Vector at the pTAKBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6JDNA."
                                      DNA.
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                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="RPCI-24-318E15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue mRNA and cDNA amplification were performed under low stringency conditions."
67 c 52 g 76 t
                                                                                                                                                    /sex="Male"
                                                                                                                                                                             /clone_lib="RPCI-24"
                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                    142
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                    137
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Pred. No. 7.8e-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              746
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                  238 t
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RPCI-24-318E15
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Query Match

8.48;

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RESULT
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Other GSSs: RPCI-24-318C15.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0200
Fax: 301 838 0200
      AZ649875
1M0519B14R Mouse 10kb plasmid
                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 318 row: C column: 15
Seq primer: SP6
Class: BAC ends.
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RPCI-24-318C15.TJ RPCI-24
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Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
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Mammalia; I
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mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(bases 1 to 796)
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/clone="RPCI-24-318C15"
/clone_11b="RPCI-24"
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/strain="C57BL/6J"
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Insert Length: 10000 Std Error: (
Plate: 0519 row: B column: 14
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Fax: 801 585 7177
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114)gb]AF129072-1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                          purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. 99 c 96 g 163 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0519B14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization for the synthesis of full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kav
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
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Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Automated filtration.5), 463-470 (1999)
system. Genome Res. 9 (5), 463-470 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 10
olfactory brain"
  was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="10 days neonate"
/lab_host="DH10B"
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/clone="E530213F07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="olfactory brain"
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
Similarity 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 433 row: L column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Other_GSSs: RPCI-23-433L3.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shao,S., Levins,M., Mcgann,S., Tsegaye,G., Geer,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS.
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AZ066617.1 GI:7357869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
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                                                                                                /note-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-433L3"
                                                                                                                                                                                                                                                                         /clone_lib="RPCI-23"
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                100.0%;
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                 Score 22;
Pred. No
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Sciurognathi; Muridae;
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K., Krol,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 496 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0508 row: M column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmalia; Eutheria; (bases 1 to 496)
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                                                                                                                                                   181
  Conservative
                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWNA2 (gi4732114)gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coil XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0508M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                           Score 22; DB 12; 
; Pred. No. 1.8;
  0,
  Mismatches
  0;
                                                  Length 496;
  Indels
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RESULT 10
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other Loss. ... Contact: Shaying Zhao
Contact: Shaying Zhao
Contact: Genomics Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Rockville,
                         BF397419 170 bp mRNA linear EUI-R-BS2-bel-b-03-0-UI.sl UI-R-BS2 Rattus norvegicus UI-R-BS2-bel-b-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.0%; 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 340 row: G column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-340G10.TV
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Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPCI-24-340G10.TJ RPCI-24 Mus musculus genomic clone RPCI-24-340G10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
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(bases 1 to 717)
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector by The BamH1; Site_2: BamH1;
/note="Vector by The BamH1; Site_2: BamH1;
/note="Vector by The BamH1; Site_2: BamH1;
/note="Vector by The BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1; Site_2: BamH1
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/clone="RPCI-24-340G10"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
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GI:11382402
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100.0%; Pred. No. 1.
1ve 0; Mismatches
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                                                                                                                                                                                                                                                                                         MI-P-E5-abn-e-02-1-UM.sl MI-P-E5 Sus scrofa cDNA clone MI-P-E5-abn-e-02-1-UM 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Madian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the ollgo-dT track served to verify it as a clone from the
normalized embryo at 13 dpc library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                       pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                 Sus scrofa
                                                                                                BF703038.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research Genetics (www.resgen.com)
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYA=Yes
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20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="embryonic 13 dpc"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT/T3D-Pac (Pharmacia) with a modified
/note="vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: Eco RI; The UI-R-BS2
library is a subtracted library derived from 13 dpc whole
embryo issue. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TRG_LIB-UI-R-BS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BS2-bel-b-03-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_TISSUE=embryo at 13 dpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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    AUTHORS
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                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 630)
                                                                                                                 potato.
Solanum tuberosum
                                                                                                                                                              EST
                                                                                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                     EST504612 cSTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized embryo at gestational day 12 library cDNA Library reparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be
                                                                                                                                                                                     BG599717.1
                                                                                                                                                                                                           BG59971
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>AT_rich#Low_complexity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Towa State University
201 Kildee Hall, Ames
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular Genetics Laboratory, Department of
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  der Hoeven, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_TISSUE=embryo at gestational day 12
TAG_SEQ=GTGAGA"
80 c 67 g 71 t
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TAG_LIB-MI-P-E5
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/clone="MI-P-E5-abn-e-02-1-UM"
/clone_lib="MI-P-E5"
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Bezzerides,J.,
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Cho, J., Chiemingo, A.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                  van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from dormant potato tubers Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG889484 630 bp mRNA ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rur cione info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Cathy Ron
                                                                                                                                                                                                                                                                                                                        Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                  For clone info: please contact Research Genetics, Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potato
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BG889484.1 GI:14266570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 630)
                                                                                                                                                                                                                                                                 primer: M13F-R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tubers
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; This library targets genes expressed in dormant
tubers. This library was made from sections of dormant
                                                                                                                                                                                   /organism="Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                            Location/Qualifiers
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                                                               /lab_host="SOLR"
                                                                              /tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
                                                                                                                          /clone_lib="cSTD"
                                                                                                                                             /clone="cSTD14C14"
                                                                                                                                                                  /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="sprouting
/dev_stage="12-14 weeks
/lab_host="SOLR"
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/cultivar="Kennebec"
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post harvest"
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cSTD14C14 5' sequence,
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark,M.; Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watarston,R.
                                                                                                                                                                                                                                                                                                                                         Seq primer: T3 ET from Amersham High quality sequence stop: 470 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (amail contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: zbrafish@watson.wustl.edu cDNA Library Arrayed cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
Other_ESTs: fd58h04.x1
Contact: Stephen L. Jo
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Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                   www.rzpd.de)
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98 c 174 g 172 t
double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I
                                        stage embry
                                                                                                                                                                                                                   /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="IMAGE:3133975"
/clone_lib="Zebrafish WashU MPIMG EST"
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                                                                                                                                                                        /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                    /sex="mixed"
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100.0%; Pred. No.
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Ostariophysi; Cypriniformes
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                                                                                                                                                                                                                         Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact red Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 120 row: F column: 14
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999) Other_GSSs: CH230-120F14.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CH230-120F14.TJ CHORI-230 Segment 1
CH230-120F14, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                            szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shaying Zhao
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                  /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-120F14"
                                                                                                                                                                                                      Location/Qualifiers
                                                              /sex="Female"
                                                                                   /clone_lib="CHORI-230 Segment 1"
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BASE COUNT ORIGIN

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173 g

162 t

Search completed: May 22, Job time: 10795 sec

2002, 07:30:25

were sequenced additional times control."

to assess quality 3 others

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by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones
                                                                                                                                                                                                                sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
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Best Local Similarity 100.
Matches 20; Conservative
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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## ALIGNMENTS

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Homo sapiens.
Synthetic.
                                                                                                                                                                                                              Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                     09-AUG-2001
20-OCT-1999;
                       20-OCT-2000; 2000WO-US29130
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The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CK (ARSACS)) gene sequences (I). The spastin gene has been mapped to CK chromosome 13q11. (I) have neuroprotective activities and can be used in CK gene therapy and as a spastin polypeptide agonists. (I), their fragments CK or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the CK diagnosis of an early onset neurodegenerative disease in an individual. CK reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CK atrophy of upper cerebellar vermis, absence of Purkinje cells and CK abnormal neuronal lipid storage. (I) can also be used to produce cantisense nucleic acids, is useful as molecular weight or chromosome CK markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for CK analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CK the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with spastin CK is derived from the human spastin nucleotide sequence (AAH20174) as stated on page 14.
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The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease conduction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnost reduced motor nerve velocity; hypermyelination of retinal nerve fibre atrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation;
                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix Saguenay disease by detecting two point mutations in spast
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WPI; 2001-308494/32.

New isolated polynucleotide, encoding spastin gene, and polypep useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in sequence polypeptides, spastin

Claim 1; Page -; 76pp; English

The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in CC gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for assaying the presence of a nucleic CC diagnosis of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, at the neurodegenerative disease. (I) can also be used to produce CC antisense nucleic acids, is useful as molecular weight or chromosome CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression correctivity of (I). The assays can be utilised to identify a subject having or at risk of developing a disease or activity. The present sequence protein or spastin gene expression or activity. The present sequence encodes a mutated human spastin.

N.B. The present sequence is not given in the present specification is derived from the human spastin nucleotide sequence (AAH20174) as stated on but

Sequence 12793 BP; 4163 Α; 2257 Ç 2487 <u>ი</u> 3886 Η. 0 other;

Query Match
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The present invention describes human and mouse spastin, and mutated CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in GC acid molecule in a sample. (I) is useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC diagnosis of an early onset neuropedepenerative disease in an individual. CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce markers, to identify genetic disorders, as hybridisation probes or CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin CC encodes a mutated human spastin nucleotide sequence (AAH20174) as derived from the human spastin nucleotide sequence (AAH20174) as
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The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purking cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or
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RESULT 7
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        The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the blagmosis of an acris contact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saquenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnos reduced motor nerve velocity; hypermyelination of retinal nerve fibratrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primers, as an antigen, identify and express recombinant protein analysis, characterisation or therapeutic use, or as markers for in which the corresponding protein is expressed. Diagnostic methothe present invention can be used to identify subjects having or of developing a disease or disorder associated with aberrant expressions.
                                                                                                                                               Claim
                                                                                                                                                                                         New isolated polynucleotide, encoding spastin gene, and puseful for diagnosing autosomal recessive spastic ataxia Charlevoix-Saguenay disease by detecting two point mutat.
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                                                                                                                                            Fig 7;
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XW Human;
XW Human;
XW autoso
KW reduce
KW atroph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnos reduced motor nerve velocity; hypermyelination of retinal nerve fibr atrophy of upper cerebellar vermis; absence of Purkinje cell;
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                                                                                                                                          New isolated polynucleotide, encoding spastin gene, and useful for diagnosing autosomal recessive spastic ataxia Charlevoix-Saguenay disease by detecting two point mutat
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                                                                                                                                                                                                                                                                                                                  Engert J,
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                                                     76pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer SEQ
                                                                                                                                                                                                                                                                                                                     Richter A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                mutations
                                                                                                                                                                                                  and polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on; diagnosis;
nerve fibre;
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                                                                                                                                             in spastin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein or spastin gene expression or activity. AAH20122 to AAH20173 represent specifically claimed primers which can be used in diagnostic methods from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human spastin ORF PCR primer SEQ ID NO:43.
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                                                                       WPI; 2001-308494/32
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                                                                                                                                                                                                           (UYMC-) UNIV MCGILL.
(HOPI-) HOPITAL SAINTE-JUSTINE
                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer; ss.
                                                                                                                                                                                                                                                                                                                   20-OCT-1999;
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                                                                                                                                           Engert J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipid storage;
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                                                                                                                                           Richter
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 21;
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New isolated polynucleotide, encoding spastin gene, and polypeptides,

(UYMC-) UNIV MCGILL

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, as an antigen, identify and express recombinant protein for a primers, as an antigen, identify and express recombinant protein for
                                                                                                                                                                                                                                                                Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory neconduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; absormal neuronal lipid storage; genetic disorder; characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. AAH20122 to AAH20173 represent specifically claimed primers which can be used in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations
                                                                                                                                                                                                                                                PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
                                     20-OCT-1999;
                                                                       20-OCT-2000;
                                                                                                               26-APR-2001
                                                                                                                                                     WO200129266-A2
                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                      Human spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH20152 standard; DNA;
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                                                                       2000WO-US29130
                                                                                                                                                                                                                                                                                                                                                                                                      ORF PCR primer SEQ ID NO:45.
                                   99US-0160588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC (ARSACS)) gene sequences (I). The spastin gane has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in CC chromosome 13q11. (I) have neuroprotective activities and can be used in CC gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the CC diagnosis of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce CC antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC in represent invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression CC constitute of (I). The assays can be utilised to identify a subject CC methods from the process of developing a disease or disorder associated with Spastin constitute of the present invention or activity. AAH20123 to AAH20173 CC methods from the present invention or activity as be used in diagnostic constitutes of the present specifically claimed primers which can be used in diagnostic constitutes the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
       WO200129266-A2
                                                                                                                                           Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnos reduced motor nerve velocity; hypermyelination of retinal nerve fibr atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                    Synthetic
                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                           AAH20154;
                                                                                                                                                                                                                                                                                                                                                                             AAH20154 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hudson TJ,
                                                                      Homo sapiens
                                                                                                                               abnormal neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOPI-) HOPITAL SAINTE-JUSTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679 gcatcagacagaatggtccag
                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gcatcagacagaatggtccag 21
                                                                                                             primer;
                                                                                                                                                                                                                                                                 spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 7; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engert J,
                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                             lipid storage;
                                                                                                                                                                                                                                                               PCR primer SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                             genetic
                                                                                                                                                                                                                                                                 ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                diagnosis;
rve fibre;
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ABL25800/c

ABL25800 standard;

DNA;

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Matches

Conservative

0;

Mismatches

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100.0%;

Score 20; Pred. No.

DB 22; 15; hes 0;

Length 20;

1174 gtgaatggccactttgcact 1193

1 gtgaatggccactttgcact 20

Query Match
Best Local Similarity

ABL25800; 26-MAR-2002

(first entry)

Drosophila melanogaster genomic polynucleotide

WO200171042-A2

Drosophila melanogaster

pharmaceutical;

developmental

biology;

cell signalling;

SEQ ID

ö

gene;

ds.

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CC acid molecule in a sample. (I) is useful for diagnosing or alding in the Cd diagnosis of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce antisease nucleic acids, is useful as molecular weight or chromosome. CC markers, to identify genetic disorders, as hybridisation probes or CC primers, as an antigen, identify and express recombinant protein for CC canalysis, characterisation or therapeutic use, or as markers for tissues CC in which the corresponding protein is expressed. Diagnostic methods from CC the present invention can be used to identify subjects having or at risk CC of developing a disorder associated with aberrant expression CC correction or sactivity of (I). The assays can be utilised to identify a subject CC having or at risk of developing a disorder associated with Spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                           (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
Sequence
                                                                 protein or spastin gene expression or activity. AAH20122 represent specifically claimed primers which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Fig 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hudson TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1999;
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                                              from the
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  BP;
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4 A;
                                         present invention.
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5 C;
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5
G;
  6 T;
  0 other;
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RESULT 13
AAF66282/c
ID AAF662
XX AAF662
XX O9-APR
XX Human;
KW breast
XX Homo s
XX Homo s
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Best L
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      Williams
Reinhard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000;
11-JUL-2000;
                                                                 (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter
                                                                                                                             02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                    WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                       breast
                                                                                                                                                                                                                                                                                                                                                                                                              Novel human polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF66282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF66282 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8496 BP;
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                                                                                                                                                                                        30-JUN-2000; 2000WO-US18374
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          Human;
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                                                                                                                                                                                                                                                                                                                                                   cytostatic; gene therapy; co cancer; lung cancer; cancer
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HYSEQ INC.
      ς,
Γ.Ε.
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2000US-0614150
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      Escobedo J, Randazzo F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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99US-0142311
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      Innis N
Kennedy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
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γ GC,
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                                                                                                                                                                                                                                                                                                                                                                      colon cancer;
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      Garcia PD,
Pot D, La
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14;
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    ), Klinger
Lamson G,
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    Kassam
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RESULT 14
AAS83961/c
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XX DNA en
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KW Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Kita D, Garcia
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                   Drmanac RT, Liu C,
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DB; ABG19774.
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2000US-0649167
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LW, Strache-Crain B;
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at the invention of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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(I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communication of the communic
Novel polynucleotides derived from Coryneform bacteria, for identifying intation point of a gene, measuring expression of a gene, analysing
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Tateishi N,
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07-APR-2000;
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analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression
  Sequence 963 BP; 220 A; 261 C;
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Matches
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                                                                                                                                                                                                                                                                                                                               Query Match
TITLE OF INVENTION: Methods and Compositions TITLE OF INVENTION: Progression FILE REFERENCE: UCSF-020/01US CURRENT APPLICATION NUMBER: US/09/156,316 CURRENT-FILING DATE: 1998-09-18
                                                                             APPLICANT: Bernstein, Harold S. APPLICANT: Coughlin, Shaun R.
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/O
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-661-6240
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NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
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TOPOLOGY: 11
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                            NUMBER OF SEQ ID NOS:
SEQ ID NO 57
LENGTH: 20
                                                                                                                                                                                                        Sequence 57, Application US/09467642 Patent No. 6300132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 11
LENGTH: 2837
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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                                                                                APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION
FILE REFERENCE: RTS-0106
CURRENT APPLICATION NUMBER: US/09/467,642
CURRENT FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 18
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                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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280 agacagaatggtccaga 296
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Local Similarity 100.0%;
nes 17; Conservat;...
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                    ON: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 RTS-0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (176373)
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Pred. No.
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Pred. No.
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RESULT 7
US-08-368-704C-12
; Sequence 12, Application US/08368704C
; Patent No. 6087160
; GENERAL INFORMATION:
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-642-57
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Best Local Similarity luv.
"^+^hes 16; Conservative
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Matches 16; Conserv
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                                                                                                                                                                                 Query Match
Best Local (
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/08/
APPLICATION NUMBER: US 08/08/
ETILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                          1366 cccctattcatgttgt 1381
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1156 actgggctgccatttc 1171
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                                                                                                           168 CCCCTATTCATGTTGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                269 base pairs
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1100 New York Avenue,
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                                                                                                                                                                   Conservative
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Pred. No.
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hes 0;
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hes 0;
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RESULT 8
US-08-991-789A-224/c
; Sequence 224, Application US/08991789A
; Patent No. 6225034
; GENERAL INFORMATION:
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US-08-368-704C-12
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TELEFAX: (202) 371-25
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bugaisky, Lawrence B.
REGISTION NUMBER: 35,086
REFERENCE,DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 01
FILING DATE: 24-JUN-1993
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APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-TOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
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FILING DATE: 4-JAN-1995
CLASSIFICATION: 435
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                                                                                                      NUMBER OF SEVENIES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed IP Law Group

ADDRESSEE: Avenue, Suite 6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAS
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                              APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTATTCATGTTGT 183
                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                                                                                         Smith, John M. Reed, Steven G.
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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US-09-062-451-224/c
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Best Local S
                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1052-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 224
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                 STRANDEDNESS:
                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                 LENGTH:
COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: POtter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (26) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/991,789A FILING DATE: 11-Dec-1997 CLASSIFICATION: <UNKnown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                               98104-7092
                            : 345 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                               Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 345 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, John M.
Smed, Steven G.
Reed, Steven G.
VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: COMPOSITIONS AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frudakis, Tony N.
                                                                                                                                                                                                                                                                                          PatentIn Release #1.0,
 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEED and BERRY LLP
                                                                                                                                                                                                                                        04-APR-1997
               single
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100.0%; Pr
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 Fifth Avenue
                                                                                                                                                                                                                                                                                          Version #1.30
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                                                                                                                            ; LOCATION: 84..302
; OTHER INFORMATION:
PCT-US91-08177-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-062-451-224
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Best Local Similarity
Matches 16; Conserv
                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application PC/TUS9108177 GENERAL INFORMATION:
                                                                                Query Match
                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Bovine resolratory syncytial virus
STRAIN: A 51908
                                                                                                                                                                                                                                          MOLECULE NYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes NUMBER OF SEQUENCES: 19
              535 ttggatgcagatttta 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 GAAAAAATTTCTATTT 168
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25 TTGGATGCAGATTTTA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., suite 1000
                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                468 base pairs
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                                                       Conservative
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                                                                    Score 16;
Pred. No.
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Pred. No.
                                                       Mismatches
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. 1.2e+02;
                                                                                  DB 5;
                                                                    1.2e+02;
                                                                                  Length 468;
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US-08-975-316-37 ; Sequence 37, Appli ; Patent No. 5952486

Application US/08975316

GENERAL INFORMATION:

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US-07-688-352C-17

; Sequence 17, Application US/07688352C

; Patent No. 5527896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                               APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               751 aatcacatggaaaaaa 766
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CTTY: Seattle
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                                                                                                                                                                                                                                                                                                                                                             755 AATCACATGGAAAAA 770
                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-269-0563
                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/975,316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
Chicago
:: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLEATH, Janet
                                     Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777 base pairs
                                                      Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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v 100.0%; Pr
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RESULT 13
US-08-474-379C-17
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                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLOPPY COMPATIBLE
COMPUTER: PATENTIAN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08474379C Patent No. 5977305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NOWBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/3019
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1299 base pair
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    960 tgaaggaaatcttact 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686 TGAAGGAAATCTTACT 701
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: 19910419
                                                                                                                                                                                                                                                                                               CITY: Chicago
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                APPLICATION NUMBER: US 07/511,715
                                                                                                                                                                                                                                         ZIP: 60606-6402
                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                             Illinois
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SYSTEM: PC-DOS/MS-DOS
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20-APR-1990
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                                                                                                                                                                                                                                                                                                                    Drive/6300 Sears
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TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: Clough, David W. REGISTRATION NUMBER: 36,

36,107

27866/32771

TELEPHONE:

(312) 474-6300

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/206,188 FILING DATE: 01-MAR-1994

APPLICATION NUMBER: US 0 FILING DATE: 19-APR-1991

US 07/688,352

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US-09-146-249A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION UDATA:
APPLICATION UNMBER: US 07/511,715
FILING DATE: 20-APR-1990
                                                                                                                                                                                                                                                                                                      ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                     SEQUENCE CHARACTERISTICS:
                                                                              NAME: Clough, David W. REGISTRATION NUMBER: 36,107 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Clough, David w
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wigler, Michael H. APPLICANT: Colicelli, John J. TITLE OF INVENTION: Cloning b TITLE OF INVENTION: Processes
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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TELEPHONE: 312-474-0448
                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Pred. No
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South Wacker Drive
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Local Similarity nes 16; Conserv

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                Query Match
Best Local :
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Matches 16; Conserv
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                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REALACTORY
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1299 base pairs
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FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/OFILING DATE: 01-MAR-1994
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                                                                                                           NAME/KEY:
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6300 Sears Tower, 233 South Wacker Drive
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score 16; DB; Pred. No. 1.2
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Search completed: May 22, 2002, 08:31:08 Job time: 6993 sec 

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Copyright (c) 1993 - 2000 Comp
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AA603783 nw66c04.s
AA639783 nw66c04.s
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## ALIGNMENTS

BASE COUNT ORIGIN REFERENCE AUTHORS VERSION KEYWORDS RESULT BM470780 LOCUS SOURCE ORGANISM COMMENT FEATURES ACCESSION DEFINITION TITLE JOURNAL source found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12218 row: k column: 16 Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC Contact: Robert Strausberg, Ph.D. 1 (bases 1 to 828)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; EST 5', mRNA sequence. BM470780 BZ8 bp mRNA linear EAGENCOURT\_6463084 NIH\_MGC\_71 Homo sapiens cDNA clone 5', mRNA seguence Unpublished (1999) BM470780.1 GI:18519822 numan cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can 262 quality sequence stop: 680. Location/Qualifiers /Organism="Homo sapiens"
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Site\_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 107 c 138 g 321 t . .828 Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. EST 05-FEB-2002 e IMAGE:5533575 þe

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REFERENCE
AUTHORS
TITLE
JOURNAL
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BE890125
LOCUS
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SOURCE
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informat found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov platg: LLAM9736 row: g column: 02
                                                                                         Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 660)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                    mRNA sequence.
BE890125
                                                                                                                             Unpublished (1999)
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/clone=lib="NIH_MGC_71"
/clone=lib="NIH_MGC_71"
/tissue_type="leionyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: uterus; Vector: pCMV-SPORT6; Site_Site_2: Sall; Cloned unidirectionally. Primer: Average insert size 2.1 kb.

a 95 c 107 g 262 t
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/db_xref="taxon:9606"
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AL567149
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The Institute for Genomic
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Plate: 255
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301 838 0208
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LTI_FL013_FBrn1
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
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Pred. No. 4.7e-91;
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EST.
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
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1 (bases 1 to 739)
Li, W.B., Gruber, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prime, mRNA sequence. AL567149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand /note="organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand /note="organ: Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: thttp://fulllength.invitrogen.com" 15 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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Pred. No. 2.2e-89;
1; Mismatches 2;
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                                                                                              aaacaaccttttctttcaatatggcatgtagtggagtttttttaacttttaaaaacatcaa
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wd27e11.x1 Soares_NFL_T_GBC_S1 F
IMAGE:2329388 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  Soares and M. Fatima Bonaldo.
86 c 70 g 167 t
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/clone_lib="Soares_NFL_T_GBC_S1"
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143 tttatgtttgtgtgtacatattttccacaaatgttataatttatatagtgtggttgaaca 202

Matches

451;

Conservative

Similarity

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Score 440; DB Pred. No. 1.7e 0; Mismatches

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Query Match Best Local

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                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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                      212
                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop:
                                                                                              /note-"Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000
                    Soares and M. Fatima
85 c 67 g
                                                           clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtr
                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:3703462"
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                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                      tissue_type="carcinoid"
                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Lu24"
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 bp
7f68a06.x1 Soares_NSF_F8_9W_OT_I
IMAGE:32997.94 3', mRNA sequence
BE856736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                            IMAGE Consortium (info@image.linl.gov)
Seq primer: -40UP from Gibco
High quality sequence stop: 448.
Location/Qualifiers
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(bases 1 to 536)
/note-Torgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002
                                                                                                                                                         /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3299794"
/clone="IMAGE:3299794"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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                                                                      Email: cgapbs-r@mail.nih.gov

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Insert Length: 1089  Std Error: 0.00
                                            Seq F
                                                                                                                                            Tumor Gene Index Unpublished (1997)
                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                         primer: -40UP from Gibco
                             quality sequence stop: 447.
Location/Qualifiers
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aatgtttgcacctccacattttattgctt
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A1803488
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 500)
                                                                               AI803488.1
                                        Homo sapiens
                                                     human.
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                                                                               GI:5368882
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/organism="Homo sapiens"

Anatomy

Project (CGAP),

Hominidae;

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KEYWORDS
SOURCE
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AW087745/c
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                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)
                                                                                                                                                                                                                                                                                  AW087745 497 bp
xb68f08.x1 Soares_NFL_T_GBC_S1
IMAGE: 2581479 3', mRNA sequence
aW087745
National Cancer
                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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//lab_host="DHIOB"
//lab_host="DH
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/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte,
pregnant uterus"
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            Institute, Cancer
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2.5e-69;
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                  Project (CGAP),
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                                                                                                                                                                        AATGTTATAATTTATATAGTGTGGTTGAACAGGATGCAATCTTTTGTTGTCTAAAAGGTGC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAGTTAAAAAAAAAACAACCTTTTCTTTCAATATGGCATGTAGTGGAGTTTTTTTAAC
A1217518 469 bp
qh20g08.x1 Soares_NFL_T_GBC_S1 I
IMAGE:1845278 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index,
                                                                                                                            593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2581479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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99.8%;
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Pred. No. 6.6e-67;
0; Mismatches 0;
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            attcatgtttgtctcgccatgcttctttacttttaacatatttctttttgcagaatgtaaaa 447
                                                                                                                                                                                                                                                                                 gcaattaagggcttacagaacatgttgaaactttttttactttttattgggaataaggaat 567
                                                                                                                                                 ggtaatgataattagtttatataagtgtactggctgtaaatgatgctaaatatactttat 507
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                                                                                                                                GGTAATGATAATTAGTTTATAAAGTGTACTGGCTGTAAATGATGCTAAATATACTTTAT
                                                                                                                                                                                                 ATTCATGTTTGTCTCGCCATGCTTCTTTACTTTAACATATTTCTTTTGCAGAATGTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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AI217518.1 GI:3797333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1845278"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 374; DB 9; 1
Pred. No. 3.3e-60;
0; Mismatches 0;
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                                                                                                                                                                                 tggaaactgcttgccaagacaacatttattaactgttagaacacttgctttatgttttgtg
                                                                                                                                                                                                                                                                                                      368 bp
ae81b08.s1 Stratagene schizo brain
IMAGE:970551 3', mRNA sequence.
AA683013
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1 (bases 1 to 368)

1 (bases 1 to 368)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University Scho
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Fax: 314 286 1810
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/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
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100.0%; Pr
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The WashU-Merck EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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Mammalia; Eutheria;
1 (bases 1 to 483)
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Seq primer: m13 -40 forward
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                    double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)."
                                                                                                                                      /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: lat strand cDNA was primed with a Not I - oligoprimer [5'
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:3897950"
/db_xref="taxon:9606"
/clone="IMAGE:279574"
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                                          4 multiple sclerosis ovided by Dr. Kevin
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                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov) for
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 422)
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1678377"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                       /tissue_type="Pooled human melanocyte, fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:3413141
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93.6%;
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Primates;
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IMAGE:1678377
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                                                                                     cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2008 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 393.
                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AA954825
                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mall.nih.gov
Tissue Procurement: L. Jeffrey Me
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                               AA954825
oo99d10.s1 NCI_CGAP_Kid6
                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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a 64 c 54 g 135 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clohe="IMAGE:1574323"
/clohe=lib="NCI_CGAP_Kid6"
/sex="mixed"
                                                                            Location/Qualifiers
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Pred. No. 4.7e-5;
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IMAGE:1574323 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330;
                                                                                        Email: estewatson.wustl.edu

Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL;

This clone is available royalty-free through LLNL;
                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                     Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                    ,R., Williamson,A.,
The WashU-Merck EST
                                                                                                                                                                                                                                                 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 418)
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                                                          IMAGE Consortium (info@image.llnl.gov)
Seq primer: m13 -40 forward
High quality sequence stop: 390.
                                                                                                                                                                                                                                                                                                                                                                                                            N46342.1
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="rogan: kidney; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5
GAATTCGGACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 |
a 64 c 51 g 133 t
/organism="Homo sapiens"
/db_xref="GDB:3897634"
                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
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Pred. No. 5.3e-52;
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Search completed: May 22,
Job time: 4096 sec
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Best Local Similarity
Matches 339; Conserv
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                                                                 CTAAATATACTTTATGCGAATTAAGGGCTTACAGAACATGTTGAAACTTTTTTTACTTTT 119
                                                                                                                                                                            CAGAACTGACATTTAATTCATGTTTGTCCCGCCATGCTTCTTTACTTTAACATATTTCTT 239
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host-"DHIOB (ampicillin resistant)"
/note-"Vector: pT/T3D (Pharmacia) with a modified
/note-"Vector: pT/T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
/ 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:279258"
/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                    55.2%;
             2002, 05:31:36
                                                                                                                                                                                                                                                                                                                                                                                                    Score 327.4; DB 10; Length Pred. No. 1.6e-51; 0; Mismatches 2; Indels
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Maximum Match 100%
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U37541 Drosophila
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                                                                                                                             TITLE
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                                                                                                                                                                                                                                  Homo sapiens adult male brain SK plus clone:hk03632.
Homo sapiens
2 (bases 1 to 4318)
Ohara,O., Suyama,M.,
Direct Submission
                                                     Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 5 (5), 277-286 (1998)
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AB018273
AB018273.1 GI:3882180
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                    Ishikawa, K. and Kikuno, R.
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partial cds
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593; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax:+81-438-52-3914)
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FFVPPTFKSVGNPVEARRWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAAD
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/clone_lib="pBluescriptII
/dev_stage="adult"
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/clone="hk03632"
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/db_xref="taxon:9606"
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tive 0; Mismatches 0;
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.jp, Tel:+81-438-52-3913,
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                                                                                       atcaaaaattgttaaaaatcattgtgttatctagtagtttataattatcggcttatatttc
                                                                                                                         AAAAAAAACAACCTTTTCTTTCAATATGGCATGTAGTGGAGTTTTTTTAACTTTAAAAAAC
                                                                                                                                    aaaaaaaacaaccttttctttcaatatggcatgtagtggagtttttttaactttaaaaac
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Hudson, T.J., Engert, J. and Richter, A. Identification of arsacs mutations and Patent: WO 0129266-A 1 26-APR-2001; McGILL UNIVERSITY (CA); Hopital Sainte Location/Qualifiers
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1 from Patent WO0129266
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital 1650 Cedar Ave., Montreal, QC H3G 1A4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richter, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bouchard, J.P., Mathieu, J., Melancon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A. ARSACS, a spastic ataxia common in northeastern Quebec, by mutations in a new gene encoding an 11.5-kb ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Engert, J.C., Berube, P., Mercier, J., Dore, C.,
Bouchard, J.P., Mathieu, J., Melancon, S.B., Sc
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Nat. Genet. 24 (2), 120-125 (2000)
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 12793)
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                                                                                                                                                          QSSEGKMTLKKIKWVPACKERPPNYPGSLVWKGDLCNLCAPPDMCDVGHAILIGSSLP
LVESIHVNLEKALGIFTKPSLSAVLKHFKIVVDWYSSKTFSDEDYYQFQHILLEIYGF
MHDHLNEGKDSFRALKFPWVWTGKKFCPLAQAVIKPIHDLDLQPYLHNVPKTMAKFHQ
                                                                 WLKVPCLSTRLINPENMGFEQSGQREPLTVRIKNILEEYPSVSDIFKELLQNADDANA
TECSFLIDMRRNMDIRENLLDPGMAACHGPALMSFNNSQFSDSDFVNITRLGESLKRG
                                                                                                                                                                                                                                                                                                                      /translation="MNTfWpGRELIVQWYPFDENRNHPSYSWLKMVWKNLYIHFSEDL
TLFDEMPLIPRTILEEGQTCVELIRLRIPSLVILDDESEAQLPEFLADIVQKLGGFVL
KKLDASIQHPLIKKYIHSPLPSAVLQIMEKMPLQKLCNQITSLLPTHKDALRKFLASL
QQKRLRKFPNQFKPFIDVFGCQLPLTVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY
NTADIYSLVDEFSLCGHRLIIFTQSVKSMYLKYLKIEETNPSLAQDTVIIKKKSCSSK
                                                                                                            LFKYCGSIEELTSDHISMYIQKIYLKSDQDLSEQESKQNLHLMLNIIRWLYSNQIPAS
PNIPVPIHHSKNPSKLIMKPIHECCYCDIKVDDLNDLLEDSVEPIILVHEDIPMKTAE
                                                                                                                                                                                                                             NPNVLEWLTPLKFIQISQEQMVSAGELFDPDIEVLKDLFCNEEGTYFPPSVFTSPDIL
HSLRQIGLKNEASLKEKDVVQVAKKIEALQVGACPDQDVLLKKAKTLLLVLNKNHTLL
                                                                                                                                                                                                                                                                           TDSSEKEKRI IQELA I FKR I NHSSDQGISSYTKLKGCKVLHHTAKLPADLRLSI SVI D
SSDEAT I RLANMLK I EQLKTTSCLKLVLKD I ENAFYSHEEVTQLMLWVLENLSSLKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SACS"
77. .11566
                                             EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMFDPNINHISKHIKDKSNPGIKINWSK
                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF31262.1"
/db_xref="GI:6907042"
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/db_xref="taxon:9606"
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PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY
RKHHLLEIGFNLVYKCDETARLYHCLIDADIFVSYVTPADIRSLMYFSSPDTNCHI
GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEENEIEVEGLFLITLDSVLQTFDAKRKF
FLTTYHELIFSRKDLEMNTLYLKYSNITLNCKVAKVFDISSFADLLSSYLPREYKTKS
CTKWKDNFASESWLKNAWHFISESVSVKEDQEETKPTFDIVVDTLKDMALLPGTKFTV
SANQLVVPEGDVLLPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSAFVP KVSEISSVPASDRAVQNLLDKLRSDGAELLMFLNHMEKISICEIDKSTGALNVLYSVK GKITDGDRLKRKQFHASVIDSVTKKRQLKDIPVQQITYTMDTEDSEGNLTTWLICNRS GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH SVDDGITLYQENITNACYKYLHEALMQNEITKMSIIDKLKPFSFILVENAYVDSEKVS FHLNFEAAPYLYQLPNKYKNNFRELFETVGVRQSCTVEDFALVLESIDQERGTKQITE ENFQLCRRIISEGIWSLIREKKQEFCEKNYGKILLPDTNLMLLPAKSLCYNDCPWIKV ACIIIKLENFMQQKV" QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT YLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSD SIPPLFSGRESHKTSSKHQSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRRL PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD NSSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPEESSQSRDSAPSTPTSPTEFLTPGLR APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR RNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRGVAFVMVEDGWKLLKPEE VVINLEYESDFKPYLYKLPLELGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ LDPNEMRTVKRVVSGLFRSLQNDSVKVRSDLENVRDLALYLPSQDGRLVKSSILVFDD MDLLSGNFLKELSLIPFLCPERAPAEFIRFHPQYQEVNGTLPLIKFNGAQVNPKFKQC DVLQLLWTSCPILPEKATPLSIKEQEGSDLGPQEQLEQVLNMLNVNLDPPLDKVINNC LESLLIIHDANSRLKQAKHFYDRTVRVFEVMLPEKLFIPNDFFKKLEQLIKPKNHVTF MTSWVEFLRNIGLKYILSQQQLLQFAKEISVRANTENMSKETLQNTVDILLHHIPQER YEVIGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLSSAEELSEIKEQLFEK LLSCHTANIESPTSILKALHYMVQTSTFRAEKLVENDFEALLMYFNCNLNHLMSQDDI KILKSLPCYKSISGRYVSIGKFGTCYVLTKSIPSAEVEKWTQSSSSAFLEEKIHLKEL VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYNCIHEDMKRLLPVVRA NQPFTEDDVRGIQNLGKGTKEGNPYKTGQYGIGFNSVYHITDCPSFISGNDILCIFDP HARYAPGATSISPGRMFRDLDADFRTQFSDVLDLYLGTHFKLDNCTMFRFPLRNAEMA KDTTVKYCHADIPREVAVKLGAVPKRHKALERYASNVCFTTLGTEFGQKEKLTSRIKS ILNAYPSEKEMLKELLQNADDAKATEICFVFDPRQHPVDRIFDDKWAPLQGPALCVYN RRLGLVPCGAVGVQLSEIQDQKWTVKPHIGEVFCYLPLRIKTGLPVHINGCFAVTSNR KEIWKTDTKGRWNTTFMRHVIVKAYLQVLSVLRDLATSGELMDYTYYAVWPDPDLVHD RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA KYSFQRFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR ALAMTLKSATDNL1SDTSYL1AMLGCND1YR1GEKLDSLGVKYDSSEPSKLELPMPGT EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL LYTAEHQDIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKEVAK LKYLKKTGSKNLCAVELPSSVKLGFEEAGCKQILLENTFSEKQFFSEVFFPNIQEIEA a 2487

BASE COUNT ORIGIN 4163 g

Query Match

Local

Similarity

100.0%; Score 593; DB 9; 100.0%; Pred. No. 3.6e-92;

Length 12793;

ρy 밁 Ş Š 밁 Ş 밁 밁 Best Loc Matches 12381 12261 12201 12321 121 181 61 ب aaaaaaaacaaccttttctttcaatatggcatgtagtggagtttttttaactttaaaaac 300 ATTTATATAGTGTGGATGAACAGGATGCAATCTTTTGTTGTCTAAAGGTGCTGCAGTTAA 12440 atttatafagtgtggttgaacaggatgcaatcttttgttgtctaaaggtgctgcagttaa 240 tattaactgttagaacacttgctttatgtttgtgtgtacatattttccacaaatgttata 180 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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                                                                                                                                                                                                                                                                               corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Ems.; EMBL; Sw:, corrections are used to associate primary accession numbers given in the feature table with their source databases: Ems.; EMBL; Sw:,
                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requests: clonerequest@sanger.ac.uk

On Apr 12, 2001 this sequence version replaced gi:12709868.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
IMPORTANT: This sequence is not the entire insert of clone RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-760Ml is at 92594 in this sequence.
                                                                                                                http://www.sanger.ac.uk/HGP/Chr13
RP11-40020 is from the library RPCI-11.1 constructed
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from 13q12.11-12.2, complete AL157766
                                                                                                                                                                                                                                                 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambri
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
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1 (bases 1 to 92693)
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                                                                                            http://www.chori.org/bacpac/home.htm
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/note="Alusq repeat:
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                                                                                                                                                                                                                                                                                           /note="Single clone region.
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                                     /note="AluY repeat: matches 1.
47477. .47873
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41541. .41788
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39790. .40093
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38703. .39008
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27150. .27653
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24769. .24891
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 /note="L1MA10
47889. .48229
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44790. .45101
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19644. .19873
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54179. .54511
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/note="AluY repeat: matches 1. .306 of consensus"
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58564. .58611
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49168. .49212
/note="Alu repeat: matches 85.
49620. .49693
/note="Alusx 72145. .72256
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55685. .55949
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52204. .53009
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62566. .62865
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61036. .61144
/note="12 repeat: matches 2581. .2696 of consensus"
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58260. .58389
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53978. .54137
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50704. .51032
                                                                  /note="MER21B repeat:
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                                                                                                                                                                                                                                                                                    note="AluY repeat: matches 136. .309 of consensus"
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/note="TIGGER1 repeat: matches 46.
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                                                                                                                                                                                                                          99819 bp DNA linear Homo sapiens chromosome UNK clone RP11-143G17, *** PROGRESS ***, 44 unordered pieces.
AC079761
2 (bases 1 to 99819)
Waterston, R.H.
Direct Submission
Submitted (10-SEP-2000)
                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 99819)
                                                              Unpublished
                                                                                The sequence of Homo sapiens
                                                                                                 Waterston, R.H.
                                                                                                                                                               Homo sapiens
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72454. .72865
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72873. .73249
/note-"MER31-internal repeat: matches 883.
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Pred. No. 2.2e-92;
; Mismatches 0;
 Genome Sequencing Center,
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                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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Pred. No. 2.2e-92;
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Tab host: TOP10
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Hashimoto, K., Osada, N.,
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Mammalia; Eutheria; Primates;
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fis (full insert sequence); oligo capping.
Macaca fascicularis adult male frontal lobe left cDNA to mRNA,
clone_lib:macaque brain cDNA library QflA clone:QflA-15307.
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/product="hypothetical protein"
/protein_id="BAB99340.1"
/protein_id="BAB99340.1"
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GLKVSCFEKLQTTLRVKGENDIPKRSETFAFLKRFGNAVILLYIQHSDSKDINFLL
LAMTLKSATDNLISDTSYLIAMLGCNDIYRIGEKLDSLGVKYDSSEPSKLELPMPGTP
                                                                                                                                                                                                               /tissue_type="frontal lobe left"
/clone_lib="macaque brain cDNA l
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                      /organism="Macaca fascicularis"
/db_xref="taxon:9541"
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R. Site1: DraIII (CACTGTGTG); R. Site2: DraIII
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Catarrhini; Cercopithecidae;
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 418)
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SSPIGKIYQIDIGYSEYXIVSSLDLYKFSRPDESSQSRDSAPSYPTSPTEFLAFGLRS
IPPLESGRESHKYTSKHOSPKKLKVNSLPEILKEVTSVVEDAWKLPESSEKKIIRKL
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KIEEYSQQLEGLTNDVHTLEAYGYDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECTA
CIIIKLENFIQQKV"
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              CTAAATATACTTTATGCGAATTAAGGGCTTACAGAACATGTTGAAACTTTTTTACTTTT
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Human STSs (1997)
Unpublished
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PCR Profile:
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Total Vol:
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/db_xref="taxon:9606"
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                                                                                                                                                      130 ttagaacacttgctttatgtttgtgtgtacatattttccacaaatgttataatttatata 189
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                     94304, USA
On Aug 12, 2000 this sequence version replaced gi:8810452.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/db_xref="taxon:5833"
/dbromosome="12"
/clone="pryAC69"
/clone="3D7"
/clone="3D7"
/clone="3D7"
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44029: gap of unknown length
87202: contig of 43173 bp in length
87402: gap of unknown length
94824: contig of 7422 bp in length
95024: gap of unknown length
95024: gap of unknown length
169794: contig of 74770 bp in length
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the places

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown

* This record will be updated with the finished sequence
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Submitted (21-MAY-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC004709
AC004709.3 GI:4558585
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14 (bases 1 to 196149)
15 (bases 1 to 196149)
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/db_xref="taxon:5833"
/chromosome="12"
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Mitochondrion Drosophila melanogaster

Mitochondrion Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of Biochemistry, Michigan State University, East Lansing, MI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L.S. Sequence, Organization and Evolution of the A+T Region Drosophila melanogaster mitochondrial DNA Mol. Biol. Evol. 11, 523-538 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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            /rpt_type=tandem
2649. .3112
/note="repeat II-A"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                          organism="Drosophila melanogaster'
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
  /rpt_type=tandem
                                                     /partia
                                                                               /note="deoxythymidylate
                                                                                                         /rpt_type=tandem
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218; Conserv
                                                 Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Eukaryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1251) to 12682)
                                                                                                                                                          Drosophila melanogaster complete mitochondrial U37541
                                                                                                                                                U37541.1
                            Wolstenholme,D.R
                                      Clary, D.O., Goddard, J.M., Martin, S.C., Fauron, C.M.
                                                                                                                      fruit fly
Nucleic Acids Res. 10 (21), 6619-6637
               Drosophila mitochondrial DNA:
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/rpt_type=tandem
complement(4565. .4585)
/note="deoxythymidylate stretch"
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/note="repeat II-B2"
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88174373
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Ballard,J.W., Olsen,G.J.,
Atkinson,P.W.
                                                                                                                                                                                                                                                                                                                                                             9 (bases 1 to 408; 13319 to 19517)

Lew1s, D.L., Farr, C.L. and Kaguni, L.S.

Drosophila melanogaster mitochondrial DNA: complunucleotide sequence and evolutionary comparisons

Insect Mol. Biol. 4 (4), 263-278 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evolutionary considerations
Genetics 118 (4), 649-663 (
                                                                                                                                                                                                                                                                              Submitted (03-OCT-1995) Laurie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L. Sequence, organization, and evolution of the A+T r Drosophila melanogaster mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified arthropods
Science 258 (5086),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evidence from 12S ribosomal RNA sequences that onychophorans
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Proc. Natl. Acad. Sci. U.S.A. 87 (24),
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Analysis of nucleotide substitutions of mitochondrial DNAs
Drosophila melanogaster and its sibling species
Mol. Biol. Evol. 4 (6), 638-650 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 5269 to 5695)
Clary,D.O., Wahleithner,J.A.
                                                                                                                                                                                                                                                                                                 Direct Submission
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171. .239
                                                                                                                                                                                                                                                                State University,
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obtained from different Drosophila melanogaster strains"
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/db_xref="taxon:7227"
                                                                                                  /product="tRNA-Ile"
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in Drosophila mitochondrial DNA: related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1345-1348 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (3), 523-538 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faith, D.P.,
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                                                                                                                                                                                                                                                              East Lansing,
                                                                                                                                                                                                                                                                              Kaguni,
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VNFITTYINMRSTGISLDRMPLFYWSVYITALLLLLSLPVLAGAITMLLTDRNLNTSF
EDPAGGDPILYQHLFWFFGHEEVYILILLGFGMISHIISQESGKKETFGSLGMIYAM
LAIGLLGFIVWAHHMETYGMDVDTRAYFTSATMIIAVPTGIKIFSWLATLHGTQLSYS
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LKSGAAPFHFWFPNMMEGLTMMNALMLMTWORLAPLMLISYLNIKYLLLISVILSVIL
GAIGGLNQTSLRKLAAFSSINHLGWMLSSLMISESTWILIFFFYSFLSFVLTFMFNIF
GKIFHLNQLFSWFVNSKILKFTLFMNFLSLGGLPFFLGFLPKWLVIQQUTLCNQYFMLT
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3907. .4068
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/note="TAA stop codon
residues to the mRNA"
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                                                                                     /product="ATPase 6"
/protein_id="AAC47815.1"
/db_xref="GI:1166534"
                                                                                                                                                                                                                                    4062. .4736
                                                                                                                                                                                                                                                                  NLNSMNWKW"
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LFFNNYVNRFLLHGQLIEMIWTILPAIILLFIALPSLRLLYLLDEINEPSVTLKSIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="cytochrome c oxidase subunit II"
/protein_id="AAC47813.1"
/db_xref="GI:1166532"
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3083. .3767
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IHWYPLFTGLTLNNKWLKSHFIIMFIGVNLTFFPQHFLGLAGMPRRYSDYPDAYTTWN
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/note="mechanism underlying r
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/db_xref="GI:1166533"
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/transl_table=5
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                                                                                                                                                                                                                                                                                                                                                                                   /product="ATPase 8"
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                                                                                                                                                                                                                                                                                              translation="MPQMAPISWLLLFIIFSITFILFCSINYYSYMPNSPKSNELKNI"
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tgctaaatatactttatgcaattaagggcttacagaacatgttgaaactttttttacttt 550
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/note="TAA stop codon is completed by the residue to the mRNA"
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VLGNIITILTVYQMWRDVSREGTYQGLHTYAVTIGLRWGMILFILSEVLFFVSFFWAF
FHSSLSPAIELGASWPPMGIISFNPFQLPLLNTAILLASGVTVTWAHHSLMENNHSQT
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complement/6/0"
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6252. .6318
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6184. .6251
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6055. .6118
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5608. .5961
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/protein_id="AAC47817.1"
/db_xref="G1:1166536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLLRHLNNHFSKNHHFGFEAAAWYWHFVDVVWLFLYITIYWWGG
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/transl_except=(pos:complement(6401.
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/protein_id="AAC47816.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence. AE001426 AE001362 AE001426.1 GI:384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erratum:[[published erratum 4;282(5395):1827]] 2 (bases 1 to 12029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gardner, M.J
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IKINKUISNEINKNOTLNDLKRSDEFHANRECSESKYVSNISAKEMTNODNC
RKSSHNKKROYSLEKELEKLYRIALAUNNYMSIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINIDNNINICHDESTYYBJILNINANSKLEEIKEKYYEVASKYHPE
KNIGANGAFKKEELINSAYQILSNEELERKYNSDGRSKMNNTHLIDPFYLFMLSYISI
NMSEYYGKLKIEYLLEESFETMNSHYDDLLLSKKIMNNYLUNYBÖKIREVELALLLERDI
ETYLEGDENCIVPIKNNIRAILEYSFSFSIMNFYGMLYEYFSKLYMGYNIELSLMNDN
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/db_xref="taxon:5833"
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/db_xref="GI:3845313"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                    Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6970686.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 7, clone RP11-661A23
                                                                                All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                             Direct Submission
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                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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Center clone name: 661_A_23
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17045 17144: gap of 100 km
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83 13489: contig of 807 bp in 16
90 13589: gap of 100 bp
90 14355: contig of 766 bp in 16
56 14455: gap of 100 bp
56 15239: contig of 784 bp in 16
10 15339: gap of 100 bp
10 15151: contig of 812 bp in 16
10 16151: contig of 812 bp in 16
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     Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Maran, B., Maran, J., Cardyna, S., Locke, K., Macdonald, P., Maran, S., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M., Maran, M.
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Birren, B., Linton, L., |
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                                                                                                                                                                                                                                          Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
SEQUENCE, 21
                                                                                                                                                                                                                                                                      Homo sapiens chromosome 4,
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/db_xref="taxon:9606"
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59712: contig of 830
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0; Mismatches
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Pred. No. 0.
                                                                                                                                                                                                                                                                      aum, C. and Lander, E. clone RP11-315D13
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McLaughlin, J.,
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COMMENT

JOURNAL

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Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6524238.
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Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 136434 bases at least Q40
Consensus quality: 115121 bases at least Q30
Consensus quality: 173987 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 181813; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
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1241 1340: gap of
1341 2108: contig of 768 bp in length
2109 2208: gap of
2209 3537: contig of 1329 bp in length
3538 3637: gap of
3638 6473: contig of 2836 bp in length
6474 6573: gap of
6574 10752: contig of 2836 bp in length
100 bp
100 bp
11053 10852: gap of
100 bp
11053 10852: gap of
100 bp
15231 15230: gap of
15331 15230: gap of
17255: contig of 4278 bp in length
17256 17355: gap of
17356 22493: contig of 5138 bp in length
17254 31215: contig of 8682 bp in length
17254 31215: contig of 8682 bp in length
17256 17315: gap of
100 bp
110 bp
121 length
12254 31215: contig of 100 bp
12254 31215: contig of 100 bp
13254 31215: contig of 100 bp
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31316 3661: contig of 4846 bp
36162 36261: gap of 100 bp
36262 43637: contig of 7376 bp
43638 43737: gap of 100 bp
43738 50536: contig of 6799 bp
50537 50636: gap of 100 bp
50637 58712: contig of 8076 bp
58713 58812: gap of 100 bp
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79132 910
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139: gap of
105647: contig
                                            31: gap of 100 bp 91039: contig of 11908 bp in
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Homo sapiens chromosome 4 clone RP11-425A23, complete sequence.
AC093835 AC027084
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University School of Medicine,
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Waterston, R.H.
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                                                                                                                  Center project name:
                                                                                                                                                   Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
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ABL33010	ABL33830	AAS46573	ABL33862	ABL33702	AAS61077	ABL32326	ABL34457	AAI76963	ABL33546	ABL33407	ABL32489	ABL34611	ABL33295	AAS45393	AAS61054	ABL32065	ABL32854	ABL33054	AAS46287	ABL32771	AAS46519	ABL33748	ABL32908	AAI76964	AAI76962	ABL33598	ABL32976	ABL26886	AAS46802	ABL32792	AAS45323	ABL33316	AAC62127	AAC62126	ABL32184
Human immune syste	Human immune syste	Tumour suppressor	Human immune syste	Human immune syste	Human gene regulat	Human immune syste	Human metastasis a	Human silent SNP c	Human immune syste	Human immune syste	Human immune syste	Human metastasis a	Human immune syste		Human gene regulat	Human immune syste		Human immune syste	Tumour suppressor	Human immune syste	Tumour suppressor	Human immune syste	Human immune syste	Human silent SNP c	Human silent SNP c	immune	Human immune syste	Drosophila melanog	Tumour suppressor	Human immune syste	Chemically pretrea		DNA encoding a cal		Human immune syste

## ALIGNMENTS

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RESULT
AAS29058
  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                 autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease; neurological disorder; gene therapy;
                                                                                                                                                                                                                       Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation; gene transcription; malignant disease;
                                                                                                                                                                                                                                                                       cDNA encoding for human DNA-binding protein #29
                                                                                                                                                                                                                                                                                             21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                       AAS29058;
                                                                                                                                                                                                                                                                                                                                           AAS29058 standard; cDNA; 1317
                                                                                  17-JAN-2001;
                                                                                                         02-AUG-2001
                                                                                                                              WO200155162-A1
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                            cytostatic; ss.
                                                                                                                                                                                      immunomodulatory; anti-HIV; anti rheumatic;
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                       2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
 2000US-0189874
2000US-0190076
                                                                                  2001WO-US01305
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anti microbial;

Human

immune immune

syste

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18-APR-2000
17-JUN-2000
28-JUN-2000
28-JUN-2000
29-JUN-2000
20-JUN-2000
11-JUL-2000
11-JUL
        2000US-0198123
2000US-0198123
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       The present invention relates proteins (AAU18154-AAU18281),
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                                                                                                                                                            WPI; 2001-465557/50
P-PSDB; AAU18182.
                                                          Claim
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                                                          SEQ
                                                                                        cid molecules encoding human secreted chromosomal binding used in preventing, treating or ameliorating a disorder, and Parkinson's diseases and cancers -
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gene their complements can be useful for assaying the presence of a nucleic cacid molecule in a sample. (I) is useful for disgnosing or aiding in the CC diagnosis of an early onset neurodegenerative disease in an individual.

The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purkinje cells and antisense nucleic acids, is useful as molecular weight or chromosome can markers, to identify genetic disorders, as hypidisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOPI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevolx-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnos reduced motor nerve velocity; hypermyelination of retinal nerve fibratrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                  N.B. The present sequence is derived from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page -;
                                                                                   encodes a mutated human spastin.
                                                                                                                                                                                                                                                                                                                                                                                                                     (ARSACS)) gene sequences (I). The spastin gene has been mapped chromosome 13q11. (I) have neuroprotective activities and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
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                                                                                                                                                                                             Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
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                                                                                                                                                                                                                  gene therapy and as a spastin polypeptide agonists. (1), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (1) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (1) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome
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          The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments cor their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for disquosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify generative as hypridisation probes or primare as an anticen identify and express recombinate protein for
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Charlevoix-Saguenay disease
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N.B. The present sequence is not given in the present specification but is derived from the human spastin nucleotide sequence (AAH20174) as
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autosomal recessive spastic ataxia of Charlevoix-Saguenay; neurodegenerative disease; reduced sensory nerve conduction
                         Human; mouse; spastin; ARSACS; chromosome 13q11;
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Best Local Similarity
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                                                                                                                     l acatcttatgtttacaggcttcctgtttgatgaagatagcaacggaaaactcaaaatggt
                                                                                                                                                                                                                                                                                                               B. The present sequence
derived from the human
tattaactgttagaacacttgctttatgtttgtgtgtacatattttccacaaatgttata
                                                  ggcagttcttattaccagttgttagtattgtttctggaaactgcttgccaagacaacatt
                                                                                                  acatcttatgtttacaggcttcctgtttgatgaagatagcaacggaaaactcaaaatggt
                                ggcagttcttattaccagttgttagtattgtttctggaaactgcttgccaagacaacatt
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HOPITAL SAII
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of upper cerebellar vermis; absence of Purkinje cell;
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                                                                                                                                                                         Conservative
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No. 9.7e-114;
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P-PSDB;
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                                                                                                                                                                                                                                                                                                           Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saquenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnos reduced motor nerve velocity; hypermyelination of retinal nerve fibr atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                              (UYMC-)
                                                                                                               20-OCT-1999;
                                                                                                                                      20-OCT-2000;
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                                                                                                                                                                                                                                                                  Synthetic
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)B; AAB97823.
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HOPITAL SAINTE-JUSTINE
                                                         Engert J,
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                                                                                                                 9908-0160588
                                                                                                                                                                                                                               Location/Qualifiers 77..11566
                                                                                                                                                                                                          /product= "mutated spastin"
                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                   storage; genetic
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isolated polynucleotide,

encoding spastin gene,

and polypeptides,

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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12793 BP; 4163 A;
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derived from the human
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100.0%; Pred. No. 9.7e-114;
tive 0; Mismatches 0;
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14-AUG-2000
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                     18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disorder; rheumatic disease; genetic infectious disease; neurological disorder; gene immunomodulatory; anti-HIV; anti rheumatic; anti
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromatin organisation modifier; Y-box binding p
DNA organisation; gene transcription; malignant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
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2000US-0229383.
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2000US-0216647.
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2000US-0217487.
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2000US-0190076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
t disease;
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2000US-0234223.
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2000US-0235884.
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2000US-0235836.
2000US-0236363.
2000US-0236367.
2000US-0236367.

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proteins (AAU18154-AAU18281), and cDNA and genomic sequences encoding CC (chromatin organisation modifier) domain proteins, and Y-box binding CC proteins may contribute to diseases resulting from aberrant DNA.
CC organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists CC that may enhance or block activities mediated by DNA-binding proteins may be useful in treating disorders CC such as malignant diseases (e.g. activities mediated by DNA-binding proteins.
CC (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid carthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzhelmer's CC diseases (e.g. HIV) and neurological disorders (e.g. Alzhelmer's CC disease). The polynucleotide sequences of the invention may also be used in gene therapy. AAS29030-AAS29157 represent cDNA sequences CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at first the printed sequence 1387 NP. 404.
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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antiinflammatory; cancer; eye disease; arteriosclerosis;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epil
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1159
                                                  Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
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2000DE-1043826
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        Human; immune system disease; cytosine methylation; antiasthy antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-Hiv; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatory; cancer; eye disease; arteriosclerosis; ana antinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy neurofibromatosis; rheumatoid arthritis; psoriasis; bowel di
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Local Similarity 46.0%;
nes 233; Conservative
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Pred. No. 0.00
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antiarteriosclerotic; antianaemic;
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for diagnosis and treatment
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01-SEP-2000;
               Human; immune system
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                                                                                                                ABL32184 standard;
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                                      system associated
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2000DE-1043826
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ment of diseases associated
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Pred. No. 0.018;
0; Mismatches 130
            cytosine methylation;
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antirheumatic; a
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01-SEP-2000;
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                                                                                                                        The present sequence encodes a polypeptide (Pf-SUB2) which has a calcium-dependent serine-protease activity. The Pf-SUB2 gene is expressed during the differentiation phase of merozoites. The protein is implicated in maturatuion of the major surface protein 1 of merozoites (MSP1-42). The enzyme is also crucial for entry of the parasite into erythrocytes. The polypeptides and polynucleotides are used to identify inhibitors of Pf-SUB2. These inhibitors e.g. antibot used for the detection, prevention, and treatment of malaria due
  4128
                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                        Polypeptide with calcium-dependent serine-protease activity, for prevention, treatment, and detection of malarial infections due
                                                                                                                                                                                                                                                                                                      WPI;
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The present sequence encodes a polypeptide (Pf-SUB2) which has a calcium-dependent serine-protease activity. The Pf-SUB2 gene is expressed during the differentiation phase of merozoites. The protein is implicated in maturatuion of the major surface protein 1 of merozoites (MSP-42). The enzyme is also crucial for entry of the parasite into erythrocytes. The polypeptides and polynuclotides are used to identify inhibitors of Pf-SUB2. These inhibitors e.g. antiboo

e.g. antibodies

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RESULT 13
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                                                                                         Nucleic acid comprising for diagnosis and treat
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01-SEP-2000;
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Plasmodium falciparum infection
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15-MAR-2000;
06-APR-2000;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                              human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3481
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell cycle; human; CpG dinucleotide; human immunodeficiency virus; neurode
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                                                                                                           15-MAR-2001;
                                                                                                                                                                                                                   WO200168911-A2
                                                                                                                                                                                                                                                                        Homo sapiens
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2000DE-1019058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation; HIV; aging;
egenerative disorder; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. 025;
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Best Local S
Matches 192
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                                                              10194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arteriosclerosis, solid
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                                                                                 gaatgtaaaaggtaatgataattagtttatataagtgtactggctgtaaatgatgctaaa
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                               tata
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192; Conserv
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2000DE-1043826
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45.38;
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Pred. No. 0.054;
0; Mismatches 232;
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                                                                                                                                                                                                                                                                                                                                    genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising frag
for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; a
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasth antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                            Sequence 19087 BP; 5469 A; 296 C; 3766 G; 9556 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 765; 32pp + Sequence Listing; German.
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL32792 standard; DNA; 19087
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  386
                                                                                                                                                                                                     tgtttgtgtgtacatattttccacaaatgttataatttatatagtgtggttgaacaggat 206
taattcatgtttgtctcgccatgcttctttactttaacatatttcttttgcagaatgtaa 445
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                               provides a number of human immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of chemically modified nent of diseases associated with
                                                                                                                                                                                                                                                         Score 52.8; DB pred. No. 0.055;
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                                                                                                                                                                                                                                                                    Length 19087;
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Listing first 45 summaries
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Match Length
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-617-860B-32
US-08-655-106-4
US-08-655-106-4
US-08-487-826B-13
US-08-991-789A-264
US-08-991-789A-264
US-08-917-755A-8
US-08-913-931C-4
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Sequence 2, Appli
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RESULT		c 45	44	43	42	41	40	39	c 38	37		c 35	34		c 32				
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	ALIGNMENTS	US-08-392-625-16	US-09-056-075-1	US-08-998-416-937	US-09-266-417-19	265-	US-09-265-315-19	US-08-714-918-19	US-08-451-405A-2	US-08-998-416-186	US-09-058-489-34	US-09-001-826-14	·US-07-867-106-2	US-08-852-629-15	US-08-852-629-11	US-08-544-332-32	US-08-107-755A-32	US-07-991-867B-32	US-08-947-823-1
		Sequence 16, Appl	Sequence 1, Appli	-	Sequence 19, Appl		Sequence 19, Appl	Sequence 19, Appl	Sequence 2, Appli	Sequence 186, App	Sequence 34, Appl	Sequence 14, Appl	Sequence 2, Appli	Sequence 15, Appl	Sequence 11, Appl	Sequence 32, Appl		Sequence 32, Appl	Sequence 1, Appli

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US-07-867-106-2/c
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU DJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
STREET: Philadelphia
                                   FEATURE:
NAME/KEY:
LOCATION:
                                                                                              TOPOLOGY: 1:
MOLECULE TYPE:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                  FEATURE:
                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                         TELEPHONE: 215-568-319
TELEFAX: 215-568-3439
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NAME/KEY:
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2378..5038
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US-07-867-106-2
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US-08-617-860B-32
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 133;
                                                                                                                                                                      APPLICATION NUMBER: DE P4329951.2
FILING DATE: 04-SEP-1993
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                             TOPOLOGY: linear MOLECULE TYPE: DN/HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                UKGANISM: Cuphea lanceolata
IMMEDIATE SOURCE:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 05-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tvpfer, R., Bautor, J., Bothmann, H., APPLICANT: Hvricke-Grandpierre, C., Klein, B., M. APPLICANT: M ller, A., Schulte, W., Voetz, M., W. APPLICANT: Schell, J.
                                                ORIGINAL SOURCE:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Promoters NUMBER OF SEQUENCES: 35
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                                                                                                                                    TYPE: N
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                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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LIBRARY genomic Lambda FIX II
                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                               1850 Base pairs
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1140 Avenue of the Americas
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                                                                                        DNA (genomic)
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, Walek, J.
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RESULT 3
US-08-605-106-4
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US-08-617-860B-32
                                                                                                                                                                                                  Sequence 4, Application US/08605106 Patent No. 5910631
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Best Local Similarity
Matches 178; Conserv
                                                                                                            GENERAL INFORMATION:
APPLICANT: Topfer, R.
APPLICANT: Martini, N.
APPLICANT: Schall, J.
APPLICANT: Schall, J.
TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TATTGAAATATTTTTTGAAATTTTAAAATATTTTTAAAATTTAAATATATTTTAAATTC 241
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LOCATION:
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LOCATION:
                                                 STREET: P.O. Box CITY: Minneapolis
               COUNTRY: UZIP: 55402
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                                        STATE: MN
                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCATTTCGGTTAAACCAAACGTAGTTCGTAACAGAATGATAAACGTGATCTATGGAAT
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1797..1799
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1642..1657
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1553..1556
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1797..1850
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1428..1432
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                                                                                  Lundberg,
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                                                                                    Woessner
                                                                                  & Kluth, P.A
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Gaps

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INFORMATION FOR SEQ ID NO: 4:
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             LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: genomic Lambda FIX II
CLONE: ClTEg1
FEATURE:
NAME/KEY: CDS
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                                                                                                                  LOCATION: FEATURE:
                                                                                                                                                           LOCATION: FEATURE:
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NAME/KEY:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNEY, WARREN D
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Cuphea lanceolata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                        LOCATION: FEATURE:
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NAME/KEY:
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NAME/KEY:
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                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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2898..3011
                                                                                                                                                                                                                                                                                                                                                                                                                                     exon II
1787..2294
exon VII
3672..3941
                                                                                                                                                                        exon V
3132..3303
                                                                                                                                                                                                                  intron IV
3012..3131
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2658..2791
                                                                                                                               intron V
3304..3390
                                                                                                                                                                                                                                                                                                       intron III
2792..2897
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2295..2657
                                                                                     exon VI
3391..3459
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1797..1799
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..3303, 3391..3459, 3672..3941)
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                                           3460..3671
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US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
- parent No. 5993827
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Best Local Similarity 44.8%;
Matches 178; Conservative
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 tgtgtacatattttccacaaatgttataatttatatagtgtggttgaacaggatgcaatc 212
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                                                                                                                                                                                         ZIP: 92660
            NAME: Israelsen, Nec
REGISTRATION NUMBER:
                                                                      FILING DATE:
                                                                                    APPLICATION NUMBER: US/08/487,826E
                                                                                                                                                                                                                                CITY: Newport Beach
                                                                                                                                                                                                                                             STREET:
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REFERENCE/DOCKET NUMBER: NIH121.001CP1
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Wellems, Thomas E.
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Pred. No. 0.019;
0; Mismatches 219;
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                                                                                                                                                                                                                                                          Sequence 7, Application US/09029213B Patent No. 6180098 GENERAL INFORMATION:
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Best Local Similarity
Matches 188; Conserv
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                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                   APPLICANT: CHRISTIAN, Peter D.
TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES
TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA
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                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             443
                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        503 tttatgcaattaagggcttacagaacatgttgaaactttttttactttt 551
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CLASSIF CATION:
                   APPLICATION NUMBER: FILING DATE: 31-AUG
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      STREET: 600 13th
CITY: Washington
                                                                                                                                              STATE:
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                                                                                                                                 COUNTRY:
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OR SEQ ID NO: 13:
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                   31-AUG-1998
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Pred. No. 0.075;
0; Mismatches 219;
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                                                                                                                                                                       Sequence 36, Application US/08883795A Patent No. 5985607
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Best Local Similarity
Matches 114; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                              APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules
TITLE OF INVENTION: Vectors for Tissue Plasmin
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                             4823 AANGTTATACATTAACATTGCTTCCAAAAATTTTTTGAGCGTCACTACTTAGAAAAT 4768
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                                                  CORRESPONDENCE ADDRESS
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NAME/KEY:
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LOCATION:
STREET: 40 Ki
CITY: Toronto
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STRANDEDNESS: doub
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                                ADDRESSEE:
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2083..2820
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4074..4875
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King Street West
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US-08-991-789A-264
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; CLONE: Rh 32
US-08-883-795A-36
                            Sequence 264, Application US/08991789A Patent No. 6225054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                     171 aaatgttataatttatatagtgtggttgaacaggatgcaatcttttgttgtctaaaggtg
                                                                                                                                                       531 gttgaaactttttttacttttattgggaata 561
                                                                                                                                                                                                                                                                                                  335 TTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAAATATTTAATTATAAACA
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                                                                                                                                                                                                                                                                                                                                                                                  291 ctttaaaaacatcaaaaattgttaaaatcattgtgttatctagtagtttataattatcgg 350
                                                                                                                              156 ATTTTAATTATAAAATATTTAATTATAAATA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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APPLICANT: Frudakis, Tony N. Smith, John M.
                                                                                                                                                                                                                                                             tctttactttaacatatttcttttgcagaatgtaaaaggtaatgataattagtttatata 470
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                     386
             STREET:
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; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-991-789A-264
                                                                                                                                                                                                                                                                       US-09-062-451-264
                                                                                                                                                                                Sequence 264, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 111; Conserv
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                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                               APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: TREATMENT AND
                                                                                                                                                                                                                                                                                                                                                                                            337 TTTCCATTCTCCCTTCCATCCTATGTNTGTCATATTTTTTCCTTTAT
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FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POTTER, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C:
TELEPHONE: (206), 622-4900
TELEPHONE: (206), 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 TTATTTTATAATTGAATTTTTTAGGATTCTATTTTATATAGATTTATCAGCTATAACACT 216
                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 292
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Seattle
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                 6300 Columbia Center,
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                                       SEED and BERRY LLP
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48.7%;
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Pred. No. 0.22;
0; Mismatches 117;
                                                                                                      AND
                     701
                                                                                                 AND METHODS FOR THE DIAGNOSIS OF BREAST CANCER
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                   Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/07991867B Patent No. 5476781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 715 base pairs
TYPE: nucleic acid
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Best Local :
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                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                      TITLE OF INVENTION: NO. 5476/Blei Entermine OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                     CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                     APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION
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NAME: Maki, David J.
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MEDIUM TYPE: Floppy disk
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                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                        COUNTRY:
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APPLICATION NUMBER: US/07/991,867B
                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atgcaattaagggcttacagaacatgttgaaactttttttacttttat 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCCATTTCTCCCTTCCATCCTATGTNTGTCATATTTTTTCCTTTAT 384
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                                                                                                                            32606
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Hall, Richard L.
                                                                                                                                          USA
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                                      PatentIn Release #1.0, Version
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NESULT 10
US-08-107-755A-8
; Sequence 8, Application US/08107755A
; Patent No. 5721352
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Best Local Similarity 47.2%;
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MOLECULE TYPE:
ORIGINAL SOURCE:
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NAME/KEY:
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REFERENCE/DOCKET NUMBER:
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DEDNESS: double
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GENERAL INFORMATION:

Moyer, Richard W.

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LENGTH: 1511 base pairs
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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APPLICATION NUMBER: US 07/827,658
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NUMBER OF SEQUENCES:
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356 atttccccatgaatgatcagaactgacatttaattcatgtttgtctcgccatgcttcttt 415
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                                                673 TGA--GTTATAATTACACATTTTTGATTAGATAAAATATATCTATTAATTTTTCGCATCA
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Local Similarity 47.2%;
les 159; Conservative
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REFERENCE/DOCKET NUMBER: UF114.C2
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
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FRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO 92/14818
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ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Stre
                              FEATURE:
NAME/KEY:
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                             FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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FEATURE:
                                                                              ORIGINAL SOURCE:
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                                                                                               MOLECULE TYPE:
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                 LOCATION:
                                                                 ORGANISM:
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Gruidl, Michael E.
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               CDS complement (18..218)
                                                                                                                unknown
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                                                                                              DNA (genomic)
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US-08-544-332-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                    ATTORNEY/AGENT INFORMATION:
                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       851 AATGGATTTACTAAATTCTGATATAATTTTAATAAAT 887
                                                                                    FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
RICH ADDITY
                                                  APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                        NAME:
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                        Meigs, J. Timothy
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No. 6239264th Carolina
                                                                                                                                                                                                                                               USA
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/ENTION: GENOMIC DNA SEQUENCES
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Steiner, Sabine
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Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                       Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Philippsen,
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Matches
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                                                                                                                                                                   APPLICANT: Bancroft, Ian
APPLICANT: Lister, Clare K
TITLE OF INVENTION: Genetic Control
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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              CURRENT APPLICATION DATA:
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                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                               CITY: Arlington
STATE: Virginia
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APPLICATION NUMBER:
                                                                                                COUNTRY:
                                                                                                                                          STREET:
                                                                                                                                                         ADDRESSEE:
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189; Conserv
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ucleic acid
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                                                                                                United States of
                                                                                                                                                                                                                             MacKnight, Richard
Bancroft, Ian
                                                                                                                                                                                                                                                         Dean, Caroline
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00 No. 6140085th Glebe
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US/08/973,273
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                            Version
                                                                                                                                           Road,
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PRIOR APPLICATION DATA:

CLASSIFICATION:

01-DEC-1997

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RESULT 14
US-09-103-478-4/c
; Sequence 4, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
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; ORIGINAL SOURCE:
; ORGANISM: Brassica
US-08-973-273-4
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Best Local Similarity
Matches 190; Conserv
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   APPLICANT:
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MS MATY J Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/GB96/01332 FILING DATE: 03-JUN-1996 PRIOR APPLICATION DATA:
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ilarity 43.3%;
Conservative
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Lotan, Tamar
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RESULT 15
US-09-193-931C-4/c
US-09-193-931C-4/c
Sequence 4, Application US/09193931C
Fatent No. 6320102
Fatent No. 6320102
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                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents Of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELECOMMUTCATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ellhorn, Gregory P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES: Townsend and Townsend and Crew LLP
ADDRESSES: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/026,221 FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/OFILING DATE: 24-JUN-1998
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77; Conserv
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52.78;
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Pred. No. 1.1;
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OTHER INFORMATION: 7.4 kb genomic wild-type fragment containing LEC1
OTHER INFORMATION: gene
NAME/KEY: misc_feature
LOCATION: (2430)..(5824)
OTHER INFORMATION: corresponds to SEQ ID NO:3
NAME/KEY: promoter
LOCATION: (2430)..(4427)
OTHER INFORMATION: corresponds to LEC1 promoter in SEQ ID NO:3
NAME/KEY: CDS
LOCATION: (4427)..(5054)
OTHER INFORMATION: LEAFY COTYLEDON1 (LEC1)
NAME/KEY: modified_base
LOCATION: (1)..(560).
OTHER INFORMATION: n = g, a, c or t
US-09-193-931C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 023070-077620

CURRENT APPLICATION NUMBER: US/09/193,931C

CURRENT FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: US 09/103,478

PRIOR PILING DATE: 1998-06-24

PRIOR PILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: US 09/026,221

PRIOR FILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: US 08/804,534

PRIOR APPLICATION NUMBER: US 08/804,534

PRIOR FILING DATE: 1997-02-21

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATCHER: 2.0

SEQ ID NO 4

LENGTH: 7560

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

FEATURE:

FEATURE: TIPEDEMATION: 7.4 % b COCCIO: 11/14-1-10-1
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Search completed: May 22, 2002, 06:34:29 Job time: 7574 sec
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                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%;
Best Local Similarity 52.7%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                             545 GAGGTTAATTTTGTAGATATTCTTTA 520
                                                                                                                                    391 catgtttgtctcgccatgcttcttta 416
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OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                           Score
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Mouse spastin nucl
Human PRO257 homol
DNA encoding novel
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## ALIGNMENTS

RESULT AAH20154

AAH20154 standard; DNA;

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AAH20154;  09-AUG-2001 (first entry)  Human spastin ORF PCR primer SEQ ID NO:47.  Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation; PCR primer; ss.  Homo sapiens.  Synthetic.
tin ORF F se; spast recessive erative d
degenerative condegenerative condegenerative condegenerative condegenerative condegenerative condegenerative co
phy of upper ce rmal neuronal l
primer; ss.
no sapiens.
nthetic.
WO200129266-A2.
26-APR-2001.
20-OCT-2000; 2000WO-US29130.
20-OCT-1999; 99US-0160588.
(UYMC-) UNIV MCGILL
(HOPI-) HOPITAL SAINTE-JUSTINE.

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Hudson

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Engert J,

Richter

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RESULT
AAH20176
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (1). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. AAH20173 represent specifically claimed primers which can be used in diagnostic methods from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or
                                                 CDS
                                                                                                                                                                     neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy and as a spastin polypeptide agonists. (1), their fra or their complements can be useful for assaying the presence of a acid molecule in a sample. (1) is useful for diagnosing or aiding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                                                                     Synthetic.
                                                                                                                                                        abnormal neuronal lipid
                                                                                                                                                                                                                           autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;
                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                        AAH20176;
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                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                              mutated spastin nucleotide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                             mouse; spastin; ARSACS; chromosome 13q11; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 A;
                                               Location/Qualifiers 77..6604
           /product= "mutated spastin"
                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
C;
                                                                                                                                                      storage; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20
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AAH20174
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome
                                                                                                                                                                                                                       N.B. The present sequence is derived from the human stated on page 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (1). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYMC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein or spastin gene expression or activity. The encodes a mutated human spastin.

N.B. The present sequence is not given in the present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to
                                                                                                       AAH20174;
                                                                                                                                       AAH20174 standard; DNA; 12793
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene sequence
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                                                                                                                                                                                                                                                                                                Similarity 100
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    resent sequence is not given in the present specificat from the human spastin nucleotide sequence (AAH20174)
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                                                                                                                                                                                                                                                                                                                                                                                     BP; 4163 A;
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                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                  Score 20; DB 2
Pred. No. 0.95;
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                                                                                                                                                                                                                                                                                                Gaps
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Human; mouse; spastin; ARSACS; chromosome 13q11; identification;

Human spastin nucleotide sequence SEQ ID NO:1.

09-AUG-2001

(first entry)

0

autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;

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                                                                                                                                                                                                acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence
                                                                                    Query Match
Best Local
                                                                    Matches
6473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                                                                                                                 Sequence 12793 BP; 4163 A; 2256 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 9; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abnormal neuronal lipid storage; genetic disorder; characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-2001
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                                                                                  Local
                                1 gtgaatggccactttgcact
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                                                                                  Similarity
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                                                                                                                                                                                     human spastin as given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engert J,
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "spastin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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Pred.
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                                                                                                 Length 12793;
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AAH20178
                                                                    markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence represents a mutated human spastin gene from the present sequence is not given in the present specification but the present sequence is not given in the present specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular verbit to rethromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ARSACS)) gene sequences (I). The spastin gene has been mapped chromosome 13q11. (I) have neuroprotective activities and can be gene therapy and as a spastin polypeptide agonists. (I), their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page -; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-308494/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of
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                                    B. The present sequence is not given in the present specification
derived from the human spastin nucleotide sequence (AAH20174) as
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page
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Query Match Best Local Similarity

100.0%;

Score 20; Pred. No.

DB 2

22;

Length 12793

Sequence

12793

BP;

4163 A;

2255

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RESULT
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or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence encodes a mutated human spastin.

N.B. The present sequence is not given in the present specification by the content of the present sequence is not given in the present specification by the content of the present sequence is not given in the present specification by the content of the present sequence is not given in the present specification by the content of the present sequence is not given in the present specification by the content of the present sequence is not given in the present sequence.
                                                                                                                             abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurodegenerative disease; reduced sensory nerve conduction; dia
reduced motor nerve velocity; hypermyelination of retinal nerve
atrophy of upper cerebellar vermis; absence of Purkinje cell;
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                                                                                                               developing a disease or disorder associated with aberrant expression
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                                                           The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments
                                                                                                                                                                                   New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                      or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual.
                                                                                                                                             Claim 1; Page -;
                                                                                                                                                                        gene sequence
                                                                                                                                                                                                                                            P-PSDB; AAB97823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is derived from the human spastin nucleotide sequence (AAH20174) as stated on page 14\,.
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The neurodegenerative

nerve velocity,

disease comprises reduced sensory nerve conduction elocity, hypermyelination of retinal nerve fibres,

atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome

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RRESULT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOLT AAHAOL
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N.B. The present sequence is not given in the present specification but is derived from the human spastin nucleotide sequence (AAH20174) as stated on page 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation; ds
                  New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix Saguenay disease by detecting two point mutations in spast
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HOPITAL SAINTE-JUSTINE.
                                                                                                                                                                                                                                     Engert J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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1..11493
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/product= "spastin"
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100.0%;
                                                                                                                                                                                                                                         Richter A;
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Pred. No. 0.95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                        point mutations in spastir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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The present invention describes human and mouse spastin, and mutated CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to CC chromosome 13q11. (I) have neuroprotective activities and can be used in GC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for assaying the presence of a nucleic CC acid molecule in a sample. (I) is useful for diagnosing or adding in the CC diagnosis of an early onset neurodegenerative disease in an individual. (CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce markers, to identify genetic disorders, as hybridisation probes or CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with spastin CC enrodes mouse enastin as alven in the present invention.
   Sequence 11493 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                 mouse
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3599 A; 2281 C;
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                                                                             in the present invention.
       2387
   G;
       3226
       <u>;</u>
       0 other;
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Matches Query Match 6397 Local Similarity nes 19; Conser 1 gtgaatggccactttgcact 20 gtgaatggccactttgctct Conservative 92.0%; 95.0%; 6416 0 Score 18.4; Pred. No. 6 Mismatches DВ 22; ۲. Length 11493; Indels 0, Gaps 0

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RESULT
ABA08683
Human
                                                                                 11-JAN-2002
                                                                                       ABA08683;
                                                                                             ABA08683 standard;
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                                                                           homologue-encoding cDNA, SEQ ID NO:459
                                                                                 (first entry)
                                                                                             CDNA; 901
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; 03-FEB-2000; 27-APR-2000; 05-FEB-2001; Homo sapiens. antifungal; vulnerary; antiulcer; cytostatic; osteopathic; vasotropic; cardiant; WO200157188-A2 2000US-0496914 2000US-0560875 2001WO-US03800 virucide; antibacterial;

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DXAXEXE
                                                                                                                                                            RESULT 9
AAS83995/c
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Best Local
DNA encoding novel human diagnostic protein #19799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides antibodies against the polypeptides, methods of detecting the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby
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                                                                                                                                          AAS83995 standard; cDNA; 1986 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening techniques. The present sequence represents novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 521-522; 1963pp; English
                                                                                               AAS83995
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 901 BP; 245 A; 182 C; 184 G; 290 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                     Local Similarity 94.
                                                                                                                                                                                                                                                                       2 tgaatggccactttgcact 20
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DB; ABB11439.
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                                                   (first entry)
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94.7%;
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Pred. No. 14;
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В
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                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                     polynocheoticles are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating in the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. AAS64197-AAS94564 represent novel human colding sequences data for this patent did not appear in the printed septence in the printed of the invention, but was obtained in electronic format directly from WIPO as the print of the invention, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                       1754 GTGAATGGCCACTCTGCA 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation pupolymerase chain reaction (PCR) primers, oligomers, and for and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, undiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to biodiversity
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P-PSDB; ABG19808.
                                         13-FEB-2002
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                                                                     AAS79251;
                                                                                                AAS79251
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention
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23-AUG-2000;
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17; Conserv
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                                                                                                 standard;
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                                       (first entry)
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2000US-0649167
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                                                                                                cDNA; 2206
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94.4%;
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maging; diagnostic; genetic (
                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                            Score 16.4;
Pred. No. 57;
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                                                                                                                                                                                                                                                                                                   438
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s useful as hybridisation probes,
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                                                                                                                                                                                                                                                                                                   464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of mutations to assess
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DNA encoding novel human diagnostic protein #15055

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RESULT 1
AAS82805/
ID AAS8
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AC AAS8
AC AAS8
DT 13-F
XX
DE DNA
XX
Huma
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CC Note: The sequence data for this patent did not appear in the printed content in the printed content in the companions.
                                                                                                                                                         В
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                                                                                                                                                                                                          Matches
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                          2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                 13-FEB-2002
                                                                                               805/c
AAS82805 standard;
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                      DNA encoding novel human diagnostic protein #18609
                                                                        AAS82805
                                                                                                                                                                                                                                                                   Sequence 2206 BP;
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                                                                                                                                                         GTGAATGGCCACTCTGCA 2028
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17; Conser
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                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                   573
                                                                                               cDNA;
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94.4%;
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Pred. No. 58;
0; Mismatches
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                                                                                               ВP
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AAS83970/c
ID AAS839
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CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences.
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23-AUG-2000;
                                                    AAS83970;
                                                                                                     AAS83970 standard; cDNA; 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2206 BP; 573 A; 638 C; 481 G;
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2000US-0649167
(first entry)
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;

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DNA encoding novel human diagnostic protein #19774.

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          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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23-AUG-2000; 2000US-0649167.
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                                                            novel human diagnostic protein #20917.
                                                                                              (first entry)
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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                    AAS88179 standard; cDNA; 2206 BP
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23-AUG-2000; 2000US-0649167
Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
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17; Conserv
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                                                              novel
                                                              human diagnostic protein #23983
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Pred. No. 58;
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RESULT 15
AAS89592/c
ID AAS89592 standard; cDNA; 2206
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CC Note: The sequence data for this patent did not appear in the printed cat for the number of the forence of the inventions.
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23-AUG-2000; 2000US-0649167.
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                                                                                   DNA encoding novel human diagnostic protein #25396.
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                                       supplement;
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DB; ABG23992.
                                                       chromosome
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17; Conserv
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                                                                                                                (first entry)
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medical imaging;
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                                       gene mapping; gene therapy;
maging; diagnostic; genetic 
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Pred. No. 58;
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Best Local :
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P-PSDB; ABG25405.
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                                                                                                                                                         Sequence 2206 BP; 573 A; 638 C; 481 G;
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-478-316-7
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US-08-478-316-7
US-08-478-316-40
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US-08-686-968C-5
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Query Match 79.0%; Best Local Similarity 89.5%; Matches 17; Conservative

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	is .	Sequence 341, Appl Sequence 37, Appl Sequence 14, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 12, Appli Sequence 23, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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                                                                                                                                            Sequence 2, Application US/08799464A Patent No. 5998601
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Best Local :
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                                                                                                                        GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
FILING DATE: NO. 5441885en
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049
APPLICATION NUMBER: 13, 199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
                              APPLICANT: Murtaugh, Michael P. et al.
TITLE OF INVENTION: VR-2332 VIRAL NUCLEOTIDE SEQUENCE AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   4880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mary Jo Boldingh
REGISTRATION NUMBER: 34,713
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 391-3383
TELEFAX: (708) 391-3356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: IMPROVED BACTERIAL STRAINS FOR
TITLE OF INVENTION: BIOREMEDIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goldberg
APPLICANT: Allenza,
APPLICANT: Lupton, I
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CITY: D
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nes 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double strand
TOPOLOGY: linear
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                     ADDRESSEE:
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2405 Grand Blvd., Suite 400
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Allenza, Paul
                                                                                                                                                                                                                                                                                                                     Conservative
                    John M. Collins
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94.1%;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (816) 474-905
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/287
FILING DATE: August 5, 199
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,26
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VR-2332 VIRAL TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474 9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 GGGAATGTCCACTTGGCACT 242
                                                                                                                                                                                       ADDRESSEE: John M. Collins
STREET: 1101 Walnut, Suite 1400
CITY: Kansas City
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                  CLASSIFICATION:
                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1..768
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                                                 APPLICATION NUMBER:
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(816) 474-9057
                                                                                   PatentIn Release #1.0, Version
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85.0%;
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/evidence= EXPERIMENTAL
/standard_name= "VR-2332 ORF
                                                  PCT/US95/09927
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Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CALHOUN,
TITLE OF INVENTION:
FOR FABRY DISEASE
                                                                                                                                                                                          Sequence 4, Application US/08478316 Patent No. 6251397
                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 07-MAY-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
       APPLICANT: PAUL, PREM S.

APPLICANT: HALBUR, PATRICK G.

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

APPLICANT: MENG, XIANG-JIN

FITTLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), PROTEIN:

TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS BASED ON THE

TITLE OF INVENTION: PROTEINS AND/OR POLYNUCLEIC ACIDS, A METHOD OF PROTECTING A

TITLE OF INVENTION: PIG FROM PRRS AND A METHOD OF DETECTING A PRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 22 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1.768
IDENTIFICATION METHOD:
OTHER INFORMATION: /evi
OTHER INFORMATION: /sta
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                                                                                                                                                                                                                                                                                                       807
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TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 328,421 FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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17; Conserv
OF SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                         76.0%;
85.0%;
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85.0%;
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/standard_name= "VR-233"
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Pred. No. 26;
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Pred. No. 23;
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                                                                                                                                                                                                                                  Sequence 5, Application Patent No. 6251397
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                APPLICANT: PAUL, PREM S.
APPLICANT: HALBUR, PATRICK G.
APPLICANT: MENG, XIANG-JIN
APPLICANT: MOROZOV, IGOR
TITLE OF INVENTION: POLYNUCLEIC
TITLE OF INVENTION: REPRODUCTION
TITLE OF INVENTION: PROTEINS AN
TITLE OF INVENTION: PROTEINS AN
TITLE OF INVENTION: PIG FROM PR
                                                                                                                                                                                                                 GENERAL INFORMATION:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4
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REGISTRATION NUMBER: 31.451
REFERENCE/DOCKET NUMBER: 4625-026-55X CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/301,435
FILING DATE: 01-SEP-1994
PRIOR APPLICATION UNMBER: US 08/131,625
FILING DATE: 05-OCT-1993
PRIOR APPLICATION UNMBER: US 08/131,625
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/969,071
FILING DATE: 30-OCT-1992
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT.
CORRESPONDENCE ADDRESS:
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                    NUMBER OF SEQUENCES:
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ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/478,316 FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcine reproductive and respiratory virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.0%;
                                POLYNUCLEIC ACIDS ISOLATED FROM A PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), PROTIEM ENCODED BY THE POLYNUCLEIC ACIDS, VACCINES BASED ON THE PROTEINS AND/OR POLYNUCLEIC ACIDS, A METHOD OF PROTECTING PIC FROM PRRS AND A METHOD OF DETECTING A PRRSV
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: PAUL,
APPLICANT: HALBUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                              TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
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APPLICATION NUMBER: 1
FILING DATE: 30-OCT-
                              NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Porcine reproductive and respiratory INDIVIDUAL ISOLATE: VR2332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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    P.C.
    1755 S. Jefferson Davis Highway, Suite 400

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                                                                                                                                                                     MENG, XIANG-JIN
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P.C.
            OBLON,
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                                            POLYNUCLEIC ACIDS ISOLATED FROM A PORCINE
REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), PROTE
ENCODED BY THE POLYNUCLEIC ACIDS, VACCINES BASED ON THE
PROTEINS AND/OR POLYNUCLEIC ACIDS, A METHOD OF PROTECTING
PIG FROM PRRS AND A METHOD OF DETECTING A PRRSV
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            SPIVAK, MCCLELLAND,
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Pred. No. 30;
              MAIER & NEUSTADT
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                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: PAUL, PI
APPLICANT: HALBUR,
APPLICANT: MENG, XI
APPLICANT: MOROZOV,
                                                                                                                                                                                                                                                                Sequence 40, Application US/08478316 Patent No. 6251397
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FILING DATE: 01-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/131,625
FILING DATE: 05-OCT-1993
PRIOR APPLICATION UNBER: US 07/969,071
APPLICATION NUMBER: US 07/969,071
FILING DATE: 310-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                      TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2352 base pairs
TYPE: nucleic acid
                                                                                      TITLE OF INVENTION:
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ORIGINAL SOURCE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                     CORRESPONDENCE ADDRESS
                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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NAME: Lavalleye, Jean-Paul M.P.
                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08 FILING DATE: 07-JUN-1995
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
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17; Conserv
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Y: U.S.A.
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                                                                                                                                                                        MOROZOV,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                OBLON,
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Jefferson Davis Highway, Suite 400
                                                                    PROTEINS
PIG FROM
: 95
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85.0%;
                                                                                      REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), PROTEI ENCODED BY THE POLYNUCLEIC ACIDS, VACCINES BASED ON THE PROTEINS AND/OR POLYNUCLEIC ACIDS, A METHOD OF PROTECTING A PIG FROM PRRS AND A METHOD OF DETECTING A PRRSV
                                   SPIVAK,
                                                                                                                                                          POLYNUCLEIC ACIDS ISOLATED FROM A PORCINE
                                                                                                                                                                             IGOR
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                                   MCCLELLAND, MAIER & NEUSTADT
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Pred. No. 30;
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COMPUTER READABLE FORM:

22202

CITY: Arlington STATE: Virginia COUNTRY: U.S.A.

MEDIUM TYPE:

Floppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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US-08-478-316-41/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-3220
TELEFAX: 248855 OPAT UR
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3293 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                 Sequence 41, Application US/08478316 Patent No. 6251397
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: PAUL, PREM S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/301,435
FILING DATE: 01-SEP-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                     APPLICANT: MOROZOV, IGOR
TITLE OF INVENTION: POLYNUCLEIC ACIDS ISOLATED FROM A PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), PROTEINS
TITLE OF INVENTION: ENCODED BY THE POLYNUCLEIC ACIDS, VACCINES BASED ON THE
TITLE OF INVENTION: PROTEINS AND/OR POLYNUCLEIC ACIDS, A METHOD OF PROTECTING A
TITLE OF INVENTION: PIG FROM PRRS AND A METHOD OF DETECTING A PRRSV
                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/969,0 FILING DATE: 30-CCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M.P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/131,625
FILING DATE: 05-OCT-1993
PRIOR APPLICATION DATA:
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                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 GGGAATGTCCACTTGGCACT 295
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                        ADDRESSEE:
3: P.C.
1755 S. Jefferson Davis Highway, Suite 400
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                                               OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
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85.0%;
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Query Match

Score 15.2;

В

Length 3295;

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RESULT 11
US-08-686-968C-5/c
; TYPE: DNA;
; ORGANISM: Porcine reproductive and respiratory syndrome virus US-08-686-968C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; INDIVIDUAL ISOLATE: US-08-478-316-41
                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 5
LENGTH: 3295
                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                    Sequence 5, Application US/08686968C Patent No. 6221361
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                       CURRENT APPLICATION NUMBER: US/08/686,968C CURRENT FILING DATE: 1996-07-25 NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                         APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               FILE REFERENCE: 39119-H/JML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/301,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
ORGANISM: Porcine reproductive and respiratory virus
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NAME: Lavalleye, Jean-Pa
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30-OCT-1992
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05-OCT-1993
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85.0%;
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Pred. No. 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Pred. No.

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US-08-799-464A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (816) 474-90 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arteriviridae (Unclassified)
STRAIN: VR-2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIA RE-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3358 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Murtaugh, Michael P. et al.
TITLE OF INVENTION: VR-2332 VIRAL NUCLEOTIDE SEQUENCE AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: un
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                                                                                                                        FEATURE:
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                                                               NAME/KEY: misc_feature
LOCATION: 1169.1701
OTHER INFORMATION: /standard_name= "VR-2332 ORF 4"
                                                                                                                                                                                                 IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "VR-2332 ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
NAME/KEY: misc_feature
LOCATION: 1716..2315
OTHER INFORMATION: /standard_name= "VR-2332 ORF 5"
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Collins, John M. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: August
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                                    NAME/KEY:
                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                       NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (816) 474-9057
                                                                                                                                                   misc_feature
624..1385
                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 August 5,
                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                                                                                                                                    /standard_name=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/799,464A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/287,941
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                                                                                                                                     "VR-2332 ORF 3"
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PCT-US95-09927-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9509927 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                  TELEFAX: (816) 474-905
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPA-
OPERATING SYSTEM: PC-DO
SOFTWARE: PATENTIN Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 261
                                                                                                                                                                                    ORIGINAL SOURCE: ORGANISM: Arteriviridae (Unclassified)
                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                     FEATURE:
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                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3358 base partype: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown
 NAME/KEY: misc_feature LOCATION: 624..1385
OTHER INFORMATION: /sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1101 Walnut, Suite 1400 CITY: Kansas City
                                    NAME/KEY:
                                                                                                                      NAME/KEY: misc_feature LOCATION: 1..768
                                                                                                                                                                   STRAIN: VR-2332
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                   3358 base pairs
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                                                                                                                                                                                                                                                                                                                                                                    (816)
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                       NO
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85.0%;
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   /standard_name= "VR-2332 ORF
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FEATURE: nisc\_feature NAME/KEY: misc\_feature LOCATION: 2303..2824 OTHER INFORMATION: /str NAME/KEY: misc\_feature LOCATION: 2817..3185 OTHER INFORMATION: /standard\_name= "VR-2332 ORF /standard\_name= "VR-2332 ORF 6" Score 15.2; Pred. No. 32; Mismatches DB 2; Length 3358; Indels 0; Gaps

0;

VR-2332 VIRAL NUCLEOTIDE SEQUENCE AND

Release #1.0, Version #1.25

IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard\_name= "VR-2332 ORF2"

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US-08-254-989-1
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LOCATION: 2817..3185
CTHER INFORMATION: /standard_name=
PCT-US95-09927-1
                                                                                     CURKENT APPLICATION UNMBER: US/08/254,989
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: US 07/830831
APPLICATION NUMBER: US 07/830831
FILING DATE: 04-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT5783
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6558
TELEFAX: (404) 815-6558
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08254989 Patent No. 5859307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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APPLICANT: Mombae
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NAME/KEY: misc_feature
LOCATION: 1169..1701
LOCATION: /st
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Papaioannou, Virginia
TITLE OF INVENTION: Mutant RAG-1 Deficient Animals Having No
TITLE OF INVENTION: Mature B and T Lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
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                    STRANDEDNESS:
TOPOLOGY: 11r
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LOCATION: 2303..2824
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| ||||| ||||||||||||
                                                                             LENGTH:
                                  nucleic acid
DEDNESS: single
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1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tonegawa, Susumu
Johnson, Randall S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mombaerts, Peter
                      linear
DNA (genomic)
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Pred. No. 3
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 5596
TYPE: DNA
ORGANISM: BAC-F2 contig 1
US-09-078-294-5
Search completed: May 22, 2002, 06:34:32 Job time: 7577 sec
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                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Mou:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4457 GGGAATGGCCTCTTTGCA 4440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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| |||||||| |||||||
                                                                                                                                 Conservative
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88.9%;
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Pred. No. 53;
                                                                                                                                              Score 14.8;
Pred. No. 59;
                                                                                                                                  Mismatches
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                        Score
         seq
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Match
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12:
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Gapop 10.0 , Gapext 1.0
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20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gtgaatggccactttgcact 20
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em_gss_inv: *
em_gss_pln: *
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gb_htc:*
gb_gss:*
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                                         238
1010
1083
621
705
299
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306
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BB624324
BB072918
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                AQ446973
AQ25211
BF944309
BF944296
BF952284
BF954333
BF944311
BF944314
BF952276
W60452276
BE652591
                                                                                                                    BM472954
BM476887
                                                                                                                                                                               SUMMARIES
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74.581 Million cell updates/sec
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                                      AA897178 am09e08.s
BM477954 AGENCOURT
BM476887 AGENCOURT
AQ44973 mgxb00021
AQ255211 mgxb0009B
BF944309 RC5-NN116
BF944296 RC5-NN116
BF944231 RC5-NN116
BF944321 RC5-NN116
BF944321 RC5-NN116
BF944314 RC5-NN116
BB624324 BB624324
BB072918 BB072918
                                                                                                                                                     Description
              BE652591 UI-M-AO0-
AZ295173 RPCI-23-1
                                W60474 zc98d08.sl
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15.8	15.8	15.8	15.8	15.8	15.8	15.8	16	16	16	16	16.4	16.4			16.4	•	16.4		16.8	•	•		•	•	•	•	
	٠	9		79.0		•	80.0		•	•		•	82.0	82.0	82.0	82.0	82.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0
378	364	358	312	297	296	154	730	627	504	425	968	654	628	593	581	581	220	825	813	712	656	639	635	618	611	601	329
12	10	12	10	9	10	12	12	12	12	12	12	12	10	10	12	10	10	10	10	9	12	10	9	9	9	10	10
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AQ923385 RPCI-23-2	BG509827 sac67d07.	BH228144 1006144E0	T86720 yd77e05.s1	AV086027 AV086027	BG220942 RST40741		BOHFE45				0		S				BG155981 saa79c09.	BF261027 HVSMEf002	BG781638 SEAUMC001	AA916846 on10f08.s		BI557012 603238477	вв589330 вв589330	AA410991 zv03a10.s	AA165498 zg49h06.r	BG624992 pgnlc.pk0	BG958614 PM4-CT080

## ALIGNMENTS

JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AA897178/c FEATURES DEFINITION LOCUS TITLE source AA897178 238 bp amn09e08.s1 Soares\_NFL\_T\_GBC\_S1 HG IMAGE:1466342 3', mRNA sequence. AA897178 AA897178.1 GI:3033798 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 238) Homo sapiens EST /note-\*Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI\_CGAP\_GCBl) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made /clone="IMAGE:1466342" /clone\_lib="Soares\_NFL\_T\_GBC\_S1" /lab\_host="DH10B" /organism="Homo sapiens" /db\_xref="taxon:9606" 1. .238 from the same 3 libraries. The pools consisted of Location/Qualifiers Homo sapiens cDNA clone

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National Institutes of Health, M
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Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:5574588"
/clone_1lb="NHL_MGC_88"
/clone_1lb="NHL_MGC_88"
/tlssue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
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Homo sapiens cDNA clone IMAGE:5574588
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mgxb0002I15f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0002I15f, DNA sequence.
             100 Jordan Hall, Clemson
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                     Clemson University
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Magnaporthe grisea
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12275 row: j column: 18
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BM476887
                                                                                                          Clemson University Genomics
                                                                                                                           Contact: Dean RA
                                                                                                                                            Unpublished (1998)
                                                                                                                                                                                                 Yu,Y., 2hu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:555441"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="NHHOB (phage resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6
Site_2: Sall; Cloned unidirectionally. P
Average insert size 2.1 kb.
4 a 219 c 212 g 318 t
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tionally. Primer: Oligo dT.
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100 Jordan Hall, Clemson Universiy, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                       Clemson University Genomics Institute
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                                                                                                                                                                                                                    Seq primer: GGAAACAGCTATGACCATGClass: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Dean RA
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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quality sequence stop: 286
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5 others
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/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
                                                                                                       /organism="Magnaporthe grisea"
/strain="70-15"
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/clone="mgxb0002I15f"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
                                       /clone="mgxb0009B20r"
/clone_lib="CUGI Rice Blast BAC Library"
                                                                                     /db_xref="taxon:148305"
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/strain="70-15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=RC5&t2=RC5-NN1163-131000-011-B11&t3=2000-10-13&t4=1)
See primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer: puc 18 forward control for the primer control for the primer control for the primer control for the primer control for the primer control for the primer control for the primer control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the following unit control for the follow
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1163-131000-011-B04&t3=2000-10-13&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 300)
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RC5-NN1163-131000-011-B04
BF944296
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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                                                                                                                                                                          /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                    tissue mRNA and cDNA amplification were performed under low stringency conditions."

92 c 90 g 50 t
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/clone_lib="NN1163"
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Fax: +55-11-2707001
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1 (bases 1 to 306)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
/clone_lib="NN1163"
/dev_stage="Adult"
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94.7%;
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Pred. No. 1.9e+02;
0; Mismatches 1;
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1 (bases 1 to 311)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
l (bases 1 to 313)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project./www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1163-
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                        Homo sapiens
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Mammalia; Eutheria; Primates;
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Seq primer: puc 18 forward
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/clone_lib="NN1163"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
This arcticate This entry can be seen in the following URL
                                                                                                                                                                    Dias Neto, E:, Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G. S., Simpson, D.H., Brunstein, A., deOliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1163-
131000-011-H03&t3=2000-10-13&t4=1)
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                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                     Contact: Simpson A.J.G
                                                                                                              sequence tags
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Ludwig Institute for Cancer Research
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Rua Prof.
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Antonio Prudente 109,
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                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1163-
101100-012-D08&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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High quality sequence stop: 315.
Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                            sequence tags
                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson, A.J
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131000-011-D08&t3=2000-10-13&t4=1)
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/dev_stage="Adult"
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sequence start: 69 sequence stop: 316
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18; Conser
                                                                                                                                                                                                                                                                                                                                                                                  Fax:
                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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                                                                                                                                                                                                                                                                                       High quality sequence stop: 340
                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97044478
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note-"Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                     /clone_lib="Pancreatic Islet"
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/db_xref="GDB:1264557"
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ORIGIN

Matches Query Match Best Local

18;

Conservative

Similarity

87.0%; 94.7%;

Score 17.4; DB 10; Pred. No. 2.2e+02;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 1-23, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE652591 477 bp mRNA UI-M-AOO-ach-d-01-0-UI.rl NIH_BMAP_MPG Mus UI-M-AOO-ach-d-01-0-UI 5', mRNA sequence.
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/lab_host="httl08 (Life Technologies)"
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/note="Vector: p
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/strain="C57BL/6J"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                       87.0%;
94.7%;
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                                                                                                     Score 17.4; DB 10;
Pred. No. 2.2e+02;
0; Mismatches 1;
                                                                                                                                                                        DB 10;
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AUTHORS
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Best Local
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447
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                                                                             Local Similarity
nes 18; Conserv
                     2 tgaatggccactttgcact 20
TGAATGGCCATTTTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea Ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 132 row: I column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Other_GSSs: RPCI-23-132I11.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Fraser, C.M. Mouse BAC End S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao
Department of Eukaryot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                             Conservative
                                                                                                                                                                                                       a
                                                                                                                                                                                                  selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).  
  135 c 94 g 201 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-23"
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94.7%;
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465
                                                                                0,
                                                                                               Score 17.4;
Pred. No. 2.
                                                                                Mismatches
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                                                                         2.4e+02;
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                                                                                                                  Length 610;
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